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Plant functional trait shifts explain concurrent changes in the structure and function of grassland soil microbial communities

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Abstract

1. Land-use intensification drives important changes to soil function and the microbial communities that regulate these, but the mechanisms underlying these changes are poorly understood as land-use can affect soil communities both directly (e.g. via changes to soil fertility) and indirectly (e.g. via changes to the quantity and quality of plant inputs).
2. Another open question is how rapidly soil microorganisms and the functions they regulate respond to environmental change. For instance, we do not know the relative importance of long-term legacies and short-term changes in land-use intensity in driving changes to microbial communities.
3. To address these topics, we measured a wide range of microbial functions, bacterial and fungal biomass and abiotic soil properties at two time intervals three years apart. This was performed in 150 grassland sites in three German regions, with sites differing greatly in management intensity.
4. Observed changes in microbial soil properties were related to both long-term means and short-term changes in: abiotic soil properties, land-use intensity index (LUI), community abundance weighted means of plant functional traits and plant biomass properties in regression and structural equation models.
5. Plant traits, particularly leaf P, and soil pH were the best predictors of change in soil microbial function as well as fungal and bacterial biomass, while LUI showed weaker impacts.
6. In most cases short-term changes, particularly to plant traits, dominated the change in soil microbial properties. However, indirect legacy effects, in which microbial change was explained by the effects of long-term LUI on plant traits, were also important. This indicates a time lag between plant community and microbial community change. Whenever effects of short-term changes in LUI were present, they acted directly on soil microorganisms.
7. Synthesis: The results suggest that soil communities and their functioning are widely resistant to short-term changes in LUI, but that they respond both rapidly and over longer time scales to changes in plant functional traits. This suggests that restoration efforts which shape and redirecting plant communities may be an effective means of managing soil communities and the functions and services they provide.

Keywords: ecosystem function, fast-slow leaf economics spectrum, hierarchical regression, land-use intensity, soil enzyme activities, soil microbial abundance, structural equation models

Introduction

Land-use intensity is a major driver of plant and soil microbial communities throughout the world's grasslands (Smith & Rushton 1994; Bossio *et al.* 1998; Keil *et al.* 2011; de Vries *et al.* 2012; Meyer *et al.* 2013). Intensification significantly impacts ecosystem processes, with major implications for the delivery of a wide range of grassland ecosystem services, including fodder production, soil carbon storage and clean water supply (Allan *et al.* 2015; Bach, Klement & Häußermann 2016; Soliveres *et al.* 2016). To date, many of the conclusions about the impacts of land-use intensification have been drawn from comparative observational studies in which the properties of high intensity sites are compared to those undergoing low intensity management (Meyer *et al.* 2013; Allan *et al.* 2015; Manning *et al.* 2015). As a result, little is known regarding the timescale over which these changes occur, the mechanisms through which such changes operate, and the relative sensitivity of different ecosystem properties to short-term changes in land use relative to long-term legacies of past land use. Furthermore, we know little of how rapidly soil microbes, which are key drivers of nutrient cycling and other soil functions, respond to changes in land-use intensity and associated changes in vegetation.

Increases to grassland land-use intensity usually operate via increased livestock densities, increased rates of fertilisation and greater mowing frequency (Blüthgen *et al.* 2012). These actions affect communities of plants and soil microorganisms and the processes they regulate through a wide range of interrelated mechanisms, which we review in brief in the following section. Initially, the physical and chemical soil environment is altered. Soil compaction by livestock and machinery can occur, not only influencing soil moisture and temperature regimes, but also reducing microbial biomass (Boeddinghaus *et al.* 2015). Furthermore, nutrient availability to both microbes and plants is increased by fertilisation, with effects on microbial communities including increases in the abundance of bacteria relative to fungi (de Vries *et al.* 2012), and a shift of microbial life strategies towards copiotrophic microbial taxa (Leff *et al.* 2015). These changes in nutrient status can also cause widespread changes to soil microbial properties and functions, including altered microbial biomass, and soil enzyme activities (Kandeler & Eder 1993; Bardgett & Leemans 1995; Donnison *et al.* 2000). A further side effect of nitrogen fertilisation in the form of reduced nitrogen is that the nitrification can lead to soil acidification (Bardgett *et al.* 1999). In turn, soil pH can affect microbial communities and soil carbon cycling (Fierer & Jackson 2006; Rousk, Brookes & Bååth 2009; Fornara *et al.* 2011). Some combination of these effects is therefore likely to be responsible for observed changes in the microbial community and its functions under grassland management intensification. However, the impact of these direct effects of intensification is accompanied by additional effects that operate via the plant community, which we term here indirect effects. High land-use intensity typically reduces plant species diversity and selects for plants with a 'fast' life history strategy (Pfestorf *et al.* 2013) typified by leaves with high nitrogen and phosphorous content, thin and/or low density, rapid turnover times and low dry matter content, reflecting low concentrations of structural compounds (Reich 2014). These traits can affect soil function by altering the chemistry and quality of litter inputs to the soil (Wardle *et al.* 2004; Orwin *et al.* 2010; Reich 2014). Accordingly, differences in 'fast-slow' traits, have been found to explain variation in soil microbial community composition and carbon storage in several studies (Wardle *et al.* 1998; Garnier *et al.* 2004; de Vries *et al.* 2012; Manning *et al.* 2015). The symbiosis between mycorrhiza and plants is also affected by soil nutrient concentrations (Treseder & Allen 2002) and the intensity of this symbiosis can be utilized as a plant functional trait (Akhmetzhanova *et al.* 2012). These community level trait changes represent an integrative measure of vegetation responses to the long-term environment (Garnier *et al.* 2004). In contrast, aboveground biomass measures reflect more a fluctuating 'snapshot' measure of vegetation response. Production typically increases in response to nitrogen addition, while belowground biomass is largely unaffected (Lee *et al.* 2010). At the same time plant cutting, e.g. through mowing, alters root exudation, which can also affect soil microorganisms (Bardgett, Wardle & Yeates 1998).

Under 'real-world' field conditions, all of the changes described above occur concurrently and are difficult to disentangle experimentally. As a result, the interrelationships between these changes have typically been examined in microcosm experiments focussing on a subset of these changes (Bardgett *et al.* 1999; Manning *et al.* 2006) and field studies are scarce. Therefore, little is known regarding the relative importance of the mechanisms described above in driving changes to soil function in 'real-world' ecosystems. However, identifying the relative roles of the pathways described here is important as it not only provides an insight into the fundamental drivers of soil systems but also allows relevant management practices to be identified (e.g. liming for pH, sowing of plant functional types).

An additional knowledge gap concerns the temporal dynamics of the changes described above. To date, most studies of temporal changes have investigated either single grassland sites over the course of a single year (e.g. Regan et al. 2017) , or studied temporal development gradients by sampling different sites in chronosequences (e.g. Kulmatiski and Beard, 2008). Such work provides limited information on the speed and magnitude of responses of communities to land-use change over intermediate (up to 10 years) timescales, especially as time lags in the response of soil microbes to land-use intensification may be common (Foster *et al.* 2003). In the case of grassland soil function for example, plant communities, and their functional properties, may take several years to fully respond to changes in land-use intensity (Poptcheva *et al.* 2009). These changes may, in turn, take time to be manifested in the activities of soil microorganisms that feed upon soil organic matter that is derived from these plants. Furthermore, recent work has argued that land-use legacies are not just important in determining current ecosystem function, but that they also play an important role in shaping responses of ecosystems to future changes (Perring *et al.* 2016). For example, the nutrient content of a soil reflects past land-use intensity and influences the effect of new nutrient inputs by determining the level of nutrient limitation of soil biota and plants (Richter *et al.* 2000; Perring *et al.* 2016). To address the knowledge gaps described above we investigated whether the functioning and composition of microbial communities rapidly tracks short-term changes (within three years) in land-use intensity or if such changes are driven by the longer-term history of the site (legacy effect). Next, we asked whether changes in soil properties and functions were best explained by direct or indirect effects of land-use intensity changes or by changes in intermediate properties, namely changes to soil pH, plant functional traits, plant diversity and the quantity and nutritional quality of plant biomass. We addressed these questions within the context of the large-scale and long-term Biodiversity Exploratories project (Fischer *et al.* 2010) by utilizing data from 150 grassland sites in three regions of Germany.

Materials and Methods

Study regions

Data were collected from 150 grassland sites spread evenly (50 each) across three regions of Germany within the framework of the Biodiversity Exploratories project (www.biodiversity-exploratories.de): Schwäbische Alb (South-West), Hainich-Dün (Central) and Schorfheide-Chorin (North-East) (see Fig. S1). All three contain protected areas, with sites spanning a full range of grassland management intensity (Fischer *et al.* 2010). The regions differ in their climate and soil types: the South-West region is a biosphere reserve on a calcareous bedrock with karst phenomena. Soils are typically shallow with bedrock typically only 10–15 cm below the soil surface and clay rich soils. The Central region also has a parent material of calcareous bedrock and clayey-loamy soil texture, while the North-East region is a young glacial landscape with predominantly sandy and organic soils. Further details on the regional characteristics are given in Table S1.

Land-use intensity

The land-use intensity, i.e. grazing intensity (number of livestock and grazing days), frequency and timing of mowing and amount and type of N-fertilizer applied, of all 150 investigated sites was assessed annually since 2006 for all 150 sites by questionnaires given to the farmers. This data was used to calculate a land-use intensity index (LUI) in which each of these three components are standardised according their full range within each region and given equal weighting (Blüthgen *et al.* 2012). The resulting LUI is a dimensionless number ranging between 0, representing no land management at all, and 4.41, very intensive land-use. Preliminary analyses showed that the LUI of the years prior to sampling (2010 and 2013) were more strongly related to soil microbial activity and biomass sampled in 2011 and 2014, respectively, than the LUI of the actual sampling years, most likely because most farming actions happened during or after the soil sampling period in spring. Therefore, the LUIs of 2010 and 2013 were chosen and the changes between these two years calculated and used for analyses.

Soil sampling

Soil samples were collected simultaneously in all three regions within two weeks in May 2011 and May 2014. All 150 grassland plots were sampled along two orthogonal transects of 20 m (Fig. S2). Sampling points were shifted by 50 cm in 2014 compared to 2011 to avoid an overlap of sampling positions. On each plot, 14 samples from 0–10 cm depth were taken using core augers. Samples were mixed, cooled and transported to a field lab, where they were sieved (< 2 mm) and frozen at -20 °C, all within eight hours of sampling.

Soil microbial analyses

Microbial biomass carbon (C_{mic}) and nitrogen (N_{mic}) were measured using the chloroform-fumigation-extraction method (CFE) of Vance et al. (1987) modified according to Keil *et al.* (2011). Microbial phosphorous (P_{mic}) was measured by combining methods by Kouno, Tuchiya and Ando (1995) and McLaughlin, Alston and Martin (1986). Details of all laboratory analyses are described in appendix 1.

Microbial functions were measured as the enzyme activities of beta-glucosidase (EC 3.2.1.21, hereafter glucosidase), beta-xylosidase (EC 3.2.1.37, hereafter xylosidase), N-acetyl-beta-glucosaminidase (EC 3.2.1.52, hereafter chitinase), phosphatase (EC 3.1.3.1) and urease (EC 3.5.1.5) as well as denitrification enzyme activity (DEA). The first four enzymes were determined by fluorescence measures in a buffered solution of pH 6.1 after Marx et al. (2001) as described in Berner et al. (2011). Urease activity was measured photometrically after Kandeler and Gerber (1988). Denitrification enzyme activity was measured according to Smith and Tiedje (1979) and Keil *et al.* (2015) after incubating the samples with substrate solution and inhibiting N_2 production with acetylene addition.

Microbial community composition, in terms of bacterial and fungal biomass, was measured using the phospholipid fatty acid (PLFA) composition of soils. Extraction was conducted following the protocol of Frostegard, Tunlid and Baath (1991) and alkaline methanolysis was performed after Dowling, Widdel and White (1986) to gain fatty acid methyl esters (FAME). According to Ruess and Chamberlain (2010) the PLFA FAMEs a15:0, i15:0, i16:0, i17:0, cy17:0, cy19:0 and 16:1ω7 represent soil bacteria, while PLFA FAME 18:2ω6,9 served as a fungal indicator. PLFA data was used to calculate the fungal to bacteria ratio (F:B). Fungal biomass was also determined as ergosterol content of bio-membranes according to a modified approach of Djajakirana, Joergensen and Meyer (1996).

Soil abiotic analyses

Soil pH was measured in 0.01 M $CaCl_2$ (1:2.5 ratio of soil: $CaCl_2$-solution). Each site was equipped with a weather station monitoring soil temperature and moisture. From this we took the mean of soil temperature from measures taken at 5 and 10 cm depth and volumetric soil moisture in 10 cm depth. Volumetric soil moisture was recalculated as percent of the water holding capacity of each plot and is referred to as soil water content (SWC) hereafter. *A priori* data analyses revealed that microbial variables were best predicted by weather data when it was calculated as arithmetic mean over a period of 30 days prior to the sampling date. These values were therefore used in subsequent analyses.

Plant data

Every year since 2008, from middle of May to middle of June, the percentage cover of all vascular plant species was estimated in a 4 m x 4 m quadrat at all sites. This data was combined with data on plant traits from the TRY database (Kattge *et al.* 2011) (for full reference list of the TRY database data see appendix 1) to calculate community abundance weighted means (CWM) of the following plant traits: specific leaf area (SLA, mm^2 g^{-1} DM), leaf phosphorous content (leaf P) and leaf nitrogen content (leaf N) both in mg g^{-1} DM. In addition, the CWM for mycorrhizal intensity (MycInt, % colonized root length) was calculated from the database of Akhmetzhanova *et al.* (2012).

Plant biomass was sampled in May 2011 and 2014 adjacent to the vegetation record by cutting the aboveground (living) plant biomass (g m^{-2}) in five 0.25 m^2 squares 2–3 cm above ground. The pooled composite sample of each site was dried (48 h at 80 °C), milled and the nutritional quality of plant biomass was measured thereafter: percent neutral detergent fibre (NDF), acid detergent fibre (ADF) and acid detergent lignin (ADL, lignin), as well as percent P and N content of the biomass were analysed using near-infrared spectroscopy (NIRS) as described in Klaus *et al.* (2016) and Kleinebecker, Klaus and Hölzel (2011). From these measures, cellulose (= ADF – ADL) and hemicelluloses (= NDF – ADF) content were calculated according to Kirchgeßner (2014).

Historic and change data

Legacy effects, *sensu* James (2015), are defined as the effects of long-term environmental conditions on the current status of a system and changes in this system in the following years. In our study legacy effects were considered those of the land-use intensity and plant functional traits that occurred up to five years before 2011, thus distinguishing them from current, short-term changes between the two sampling years: 2011 and 2014. To differentiate legacy effects of land-use intensity and plant functional traits from the effects of short-term changes in these properties, we calculated separate measures for these time periods and termed them ‘historic’ (h) and ‘changes’ (Δ) for the ecosystem variables (see Table S2 for details on the time frames which were used to calculate these categories). The changes for each variable (*y*) on each site (*i*) in between the measured years 2011 and 2014 were calculated as

$$y_{i\Delta} = (y_{i2011} - y_{i2014}) \times -1$$

with 2011 serving as base year. Historic values were calculated as the arithmetic mean over several years.

Statistical analyses

All statistical analyses were performed in R versions 3.3.2 and 3.4.2 (R Core Team 2016; R Core Team 2017). Preliminary analyses showed strong differences between the three regions for multiple variables and the confounding of several factors with region (e.g. soil texture, soil type and climate). Therefore, the three regions were analysed separately in subsequent statistical procedures.

Statistical modelling of changes in soil properties

We used a model selection approach to identify the environmental variables (historic and change measures) that best explained changes in microbial soil properties between 2011 and 2014. This was done with forward selection according to a hypothesized ‘hierarchy of controls’ in which ultimate controls of soil properties were added before proximate drivers (Díaz *et al.* 2007). In accordance to prior knowledge presented in the introduction, explanatory variables were grouped and added to the model in the following hierarchal sequence: 1) fundamental abiotic soil properties, 2) land-use intensity variables, 3) ΔpH, as fertilisation can influence the pH level, 4) measures of plant functional composition, and 5) plant biomass properties, as these are partly controlled by the functional traits and respond more rapidly to changes in growing conditions. See Table S3 for details.

Utilizing this approach, we compared a range of linear mixed effect models for every microbial response variable in each region, using the lme function of the nlme package (Pinheiro *et al.* 2017). First, spatial correlation structures were tested for their significance (i.e. exponential, Gaussian, spherical, linear spatial correlation and rational quadratics). Secondly, as it comprises many unmeasured variables, soil type was tested as a random effect. If neither correlation structure nor random factor increased model likelihood, a linear model was fitted (Crawley 2015). This resulted in only linear models in the South-West, while some models in the Central and North-East regions included spatial autocorrelation structures (five times) or soil type (four times). Variable selection was based on Akaike’s information criterion (AIC), and new variables were only retained, if they lowered AIC by >2 and were significant in a likelihood ratio deletion test ($P < 0.05$). If several variables remained in the model, their first order interaction was tested. The fit of the final model was assessed based on normal distribution and heteroscedacity of model residuals. As the range of most variables was relatively short, only linear terms were fitted. Percent of unique variance explained was calculated as R^2 after Nakagawa and Schielzeth (2013). R^2 values for each level and interaction were derived by subtracting R^2 from the model without the respective level from the R^2 of the full model.

In preliminary analyses we found that measures of plant species richness, functional diversity (Rao's Q index), a composite measure of plant traits representing the fast-slow spectrum based upon the first axis scores of a principal component analysis of CWM SLA, CWM leaf P and CWM leaf N, plant functional group identity (numbers of legumes, grasses and forbs per site) and lignin:N ratio of plant biomass were not significantly related to soil microbial processes. Therefore, these variables were omitted from the final modelling procedure.

Structural equation models

Model selection indicated that land-use intensity was not the most important driver of changes in microbial soil properties (see results). However, it is possible that effects of land-use intensity were present, but not detected, because land-use intensity was correlated with better predictors, e.g. changes to plant properties. This hypothesis was tested by using strictly confirmatory structural equation modelling (SEM) which allows direct and indirect effects to be distinguished. Due to differences between regions separate SEMs were fitted for each region. As the maximum replication was therefore 50 we limited the number of pathways to allow for reliable parameter estimation. Based on the hierarchical regression results the change and legacy effects of pH, CWM MycInt, CWM leaf P, plant biomass and its lignin content were selected as mediator variables as these were significant in model selection and, in case of CWM leaf P and plant biomass, representative of other significant plant variables (see Fig. S3 a-c). See Fig. 1 a) and b) for details of SEMs structure. Separate models were run for each microbial soil property and each of the mediator variables in the software package lavaan (Rosseel 2012). As random effects were only retained in 9 of 42 regression models simple linear regression formula were used in the SEMs. Maximum likelihood estimation was used to fit models. Model selection for the best mediator variable was based on two steps: 1) lowest AIC value, 2) if applicable, chi-square test results (lowest) and associated *p*-values ($P > 0.05$). Data were scaled between [0;1] to yield similar ranges and to allow comparison of standardized estimates between SEMs (Scherber *et al.* 2010). In the North-East region, no model could be selected because all differed significantly from the observed data co-variance matrices, most likely due to weak associations between variables (see Fig. S3 c).

Results

Changes over time

Changes in soil microbial and environmental properties between 2011 and 2014 varied greatly between sites and regions (Fig. 2a-b). Soil enzyme activities involved in C, N and P cycling, and particularly denitrification enzyme activity, were, generally higher in 2014 in all three regions (Fig. 2a). Fungal biomass increased in all three regions (PLFA means between +11% and +72%), while microbial biomass C and N changed little in the South-West and North-East, and generally declined in the Central region. Plant biomass was much higher in 2014 compared to 2011 in all regions (Fig. 2b), most likely due to the hot and dry spring of 2011, which was reflected by the overall lower soil water content and higher temperature in the 30 day period prior to sampling in the Central and North-East regions. This was accompanied by general increases in the nutritional quality of plant biomass in terms of P, cellulose, hemicellulose and lignin content, while plant biomass N either did not change (North-East) or declined (Central and South-West regions, mean values between -10% and -13%). Compared to plant biomass, the CWM of plant functional traits and LUI showed relatively smaller changes at most sites. pH changed little in the South-West and Central regions (standard deviations ~±1.5%), but moderately in the North-East (standard deviations ±5.7%).

Recent history

The historic means of pH, LUI and plant traits in each region are displayed in Fig. 2c. CWM plant traits of the fast-slow-gradient were 'fastest' in the North-East, while LUI was equally distributed across all three regions. The Central region has on average the highest historic pH values (6.9) allthough the North-East shows the widest range of pH values.

Drivers of microbial change

In all three regions model selection showed that changes in plant community properties, particularly plant functional traits, were better able to explain changes in microbial soil properties than changes in land-use intensity and environmental drivers, especially in the South-West (Table 1). However, in the Central region LUI effects were also retained in 36% of the models, and in the North-East the influence of changing pH was important (retained in 36% of the models), especially in explaining changes in enzymatic activities and the ΔC_{mic}:N_{mic} ratio.

Changes in most microbial properties were driven by just one or two explanatory variables (43% and 33% percent of all models, respectively); interactions between variables were much rarer (present in 21% of all models). Furthermore, recent changes were more often linked to the changes in microbial soil properties than legacy effects (retained in 54% and 27% of models, respectively). Of the abiotic environmental properties, it was soil pH which most often explained soil microbial changes (retained in 32% of models). In contrast, temperature had little influence (retained in 7% of models) and SWC none at all. Changes in pH did not alter soil microbial properties in the South-West and Central regions, but negatively impacted $\Delta C_{mic}:N_{mic}$-ratio and positively affected several enzyme activities in the North-East, where it also explained, on average, 16% of the unique variance.

Increases in LUI were accompanied by a reduction in fungi, in that short-term changes in LUI were negatively related to Δergosterol content in the South-West, and to Δfungal abundance in the Central region (Table 1). The contrary was found in the North-East. Legacy effects of LUI were rarely related to microbial soil properties in the South-West (only to ΔP_{mic}) and not at all in the North-East, but was retained in 29% of the models in the Central region.

Plant functional traits were the most frequently selected explanatory variables (retained in 55% of all models, and in 71% in the South-West). They also explained most of the unique variance across all hierarchical regression levels, both in the South-West and Central Region (up to 44% and 49%, respectively), thus indicating that they were important drivers of changes to soil properties. Of these, CWM leaf P was the most important functional trait and it was significantly related to soil microbial properties in all three regions. Its change and historic values were both negatively and positively related to microbial variables including: ΔC_{mic}, ΔN_{mic}, ΔP_{mic}, ΔDEA, enzyme activities of Δurease activity, Δglucosidase, Δchitinase and Δxylosidase, Δfungi:bacteria-ratio and Δergosterol content. The other plant traits had less consistently strong effects and were never important in all three regions.

Overall, plant functional traits were more important and explained more unique variance than plant biomass properties in all three regions. However, where plant biomass or its nutritional properties, i.e. cellulose and lignin content, were retained in models, their increases were consistently related to increases in soil microbial variables.

Direct and indirect land management effects

Structural equation modelling consistently selected CWM leaf P as the most likely mediator variable for every soil microbial property. The selected models showed that indirect legacy effects of historic LUI operated via historic CWM leaf P in the South-West, while in the Central region direct effects of historic LUI prevailed; Indirect effects of ΔLUI were not found at all (Fig. 3, see Tables S5.1-3 for parameter values). In the South-West and Central regions historic LUI strongly positively affected historic CWM leaf P ($r \approx 0.72$ South-West, $r \approx 0.64$ Central), but a significant connection between changes in LUI and vegetation properties was never identified.

Discussion

Our study revealed that changes in plant properties were much stronger drivers of short-term changes in soil microbial properties than either changes in, or the legacy of, land-use intensity. Of the evaluated plant variables, the CWM of plant traits, particularly CWM leaf P, explained more variance in soil microbial properties than plant biomass or its nutritional quality. However, pH change had a strong influence on changes to soil microbes and associated enzyme activities in the sandy and organic material rich soils of the North-East.

The finding that the influence of plant properties on soil microorganisms was stronger and more frequent than that of land-use intensity contrasts with studies that showed strong linkages between bacterial abundance, enzyme activities and fertilisation rates (Bardgett & McAlister 1999; Ritz *et al.* 2004). Surprisingly, as this variable has been found to relate to grassland soil properties in the past (e.g. Manning et al, 2015), plant N content, either measured as a functional trait or in biomass, showed only weak, if any, effects on changes in microbial soil properties. Instead, it was the CWM of leaf P, as either its change or as a legacy effect, that showed strong relationships with soil microbes. These relationships were also stronger than those with CWM SLA which has been shown to be strongly related to wide range of ecosystem properties (Garnier *et al.* 2004; de Vries *et al.* 2012; Allan *et al.* 2015; Manning *et al.* 2015). Among the plant traits, leaf P content correlates with SLA and leaf N, which together can characterise the fast-slow spectrum of plant growth behaviour described by Reich (2014) and Díaz *et al.* (2016). Previously, de Vries *et al.* (2012) showed a positive association between bacterial dominance and plant communities possessing ‘fast’ traits. Our own results confirm and extend this finding by demonstrating that such linkages operate over short time scales, with changes in F:B ratio tracking changes in plant community P content and other related fast-slow traits. In our study, declines in the relative abundance of fungi with increases in fast plant traits were observed repeatedly. P availability is limited under high pH (compare Fig. 2c a)) and the amount of recalcitrant P in the calcareous South-West and Central regions has been shown to be much larger than in the North-East region (Alt *et al.* 2011). This may lead to phosphate limitation in these calcareous regions, thus explaining the strong positive associations between P rich plant material that enters the soil and microbial activity, as the organic P is mineralized by phosphatase enzymes of both microbial and plant origin. Laboratory studies have shown that short term changes in soil microorganisms and soil processes are strongly linked to plant traits (Bardgett *et al.* 1999; Orwin *et al.* 2010). Our field study not only supports these findings, but also shows that the long-term history of plant traits on a site can have stronger influence on soil microorganism than land-use intensity.

We observed a large increase in plant biomass from 2011 to 2014, which was most likely linked to the fact that spring 2011 was relatively dry, resulting in a low biomass production, whereas

2014 was benign. The corresponding differences in weather conditions did not directly affect the soil microorganisms though, as effects of mean soil temperature over 30 days prior to sampling were minimal and soil moisture effects were undetectable. As plant biomass and its nutritional quality in terms of cellulose, hemicellulose or lignin content, were generally positively related to soil microbial properties, we conclude that plant growth positively influences soil microbial biomass and the speed of nutrient cycling. The observed relationship could be driven by inputs of plant material, but also by correlated increases in rhizodeposits (Swinnen, Van Veen & Merckx 1995), which demonstrated a positive association with microbial biomass (Bardgett, Wardle & Yeates 1998; Eisenhauer *et al.* 2017) and enzyme activity (Spohn, Ermak & Kuzyakov 2013). The main source of extracellular enzymes in soils are microorganisms (Das & Varma 2011), although there is a small contribution of roots and soil animals (Acosta-Martínez & Tabatabai 2011; Kandeler *et al.* 2011).

We found pronounced variation in the relative importance of different drivers of changes in microbial soil properties among the three study regions. This regional variation may be due to differences in soil conditions, namely texture, soil type and water regime. For example in the North-East, changes in microbial soil properties were often linked to changes in soil pH. This is unlikely to be a consequence of land management, e.g. liming or ammonium fertilization, as the explained variance would have been attributed to land use. Instead we suggest that the lower buffering capacity of the sandy soils made alteration in the redox-potential caused by shifts in the water regime more likely, compared to the other regions. Enzymatic activities were strongly affected by changing pH levels, which is in accordance with the importance of pH for soil enzyme activities reported by Acosta-Martínez and Tabatabai (2011). While microbial activity was affected by pH, the F:B ratio, i.e. the community composition of soils, did not respond to pH changes, likely because pH varied by a maximum of 1.6 units within a site. This small range probably explains why this finding differs from studies which found strong pH effects on microbial community composition; these reported pH values ranging from 3 to 9 (Fierer & Jackson 2006; Griffiths *et al.* 2011).

Results from all three regions, demonstrated that short-term changes in environmental, land-management and especially plant variables have important and rapid effects on soil microbial properties. Structural equation modelling added further insight to this finding by providing evidence that these changes operate directly, via changes in land management and nutrient inputs. Meanwhile, legacy effects of land-use intensity also acted, but more indirectly via plant functional traits. However short-term trait effects were the most common driver of microbial change in most cases. Our results showed that legacy effects of land-use can be strong drivers of current changes to soil microbes and their activity. However, there was little evidence that land-use legacies affected the impact of current land-use changes (Perring *et al.* 2016), as significant interactions between land-use change and land-use history were not observed. To our knowledge, we are the first study to demonstrate a legacy effect of land-use intensity on changes to the function and community composition of soil microorganisms. We suggest that plant mediated legacy effects are due to the long-term and cumulative effects of land-use intensity on plant communities which take several years to adjust to management practices. Furthermore, we hypothesise that the importance of these legacy effects in driving soil microbial changes, relative to short-term variation in land management, is due to a time lag between changes in soil microbial communities, which decompose not only fresh but also old organic material. Therefore, part of the microbial community is feeding on ‘historic’ substrates, i.e. more recalcitrant, older soil organic carbon (Müller *et al.* 2016), and this component ‘catches up’ with the land-use change and corresponding vegetation change as vegetation inputs related to more recent land-use changes enter these more slowly cycling pools.

Conclusion

By studying the changes in microbial soil properties in successive years on 150 sites in three regions together with environmental, land management and plant properties at the sites, we were able to show that vegetation change was the primary driver of changes in soil microbial communities and activities. However, regions differed in their behaviour, most likely due to variance in key properties such as climate, soil types and hydrological conditions. Wider studies across an even fuller range of conditions are required to gain a mechanistic understanding of these context dependencies. Where changes in soil microbial properties were not explained by vegetation they were driven by changes in pH. Importantly, we were able to show that legacy effects of land-use intensity can be strong and that they are mediated by functional plant traits, in particular leaf P, which was consistently the best predictor, among many, of belowground changes between years. Furthermore, this study emphasizes that while both legacy and short-term changes in the environment can drive microbial abundance, community composition and functional change that short-term changes play the greater role. Our results suggest that restoration efforts which shape and redirect plant communities may be an effective means of managing soil communities and the functions and services they provide, but that such efforts may take a long time to prove their effectiveness.

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Author Contributions:

RSB and PM wrote the manuscript. RSB, SM, BD, SB, FM, HN, JK, VHK, TK, YO, DP, DS, SI, MS, ES, EK and PM provided data. RSB analysed data. PM, EK and SM initiated the study. PM and RSB designed the analyses. All authors read and revised the manuscript.

Data accessibility:

All data used for this study are archived within the BExIS database of the Biodiversity Exploratories project, the TRY database and Ecological Archives E093-059.

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Figures

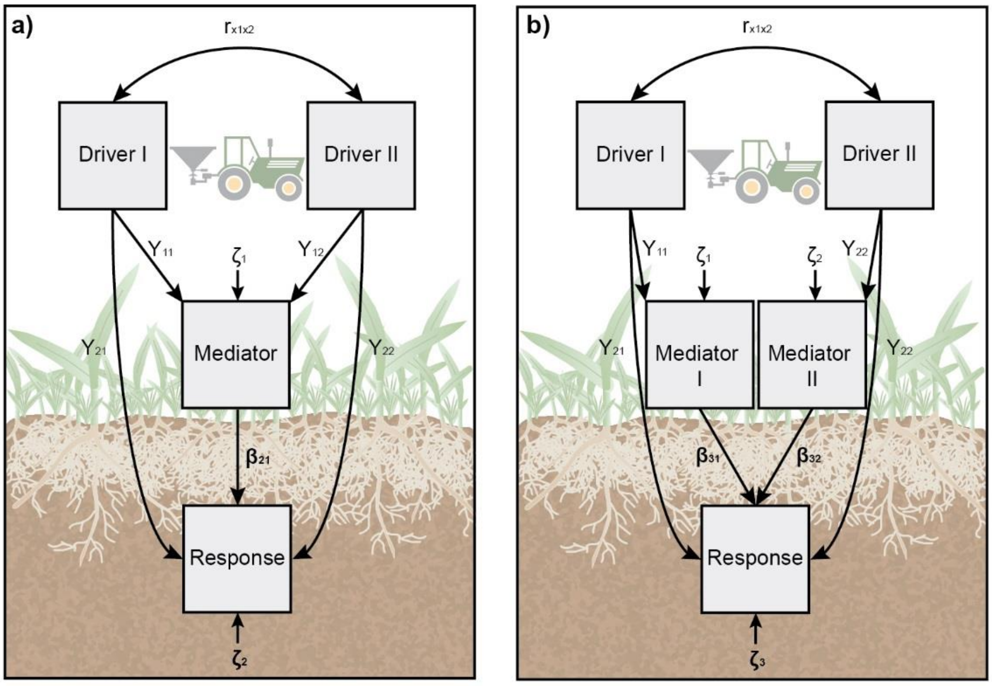
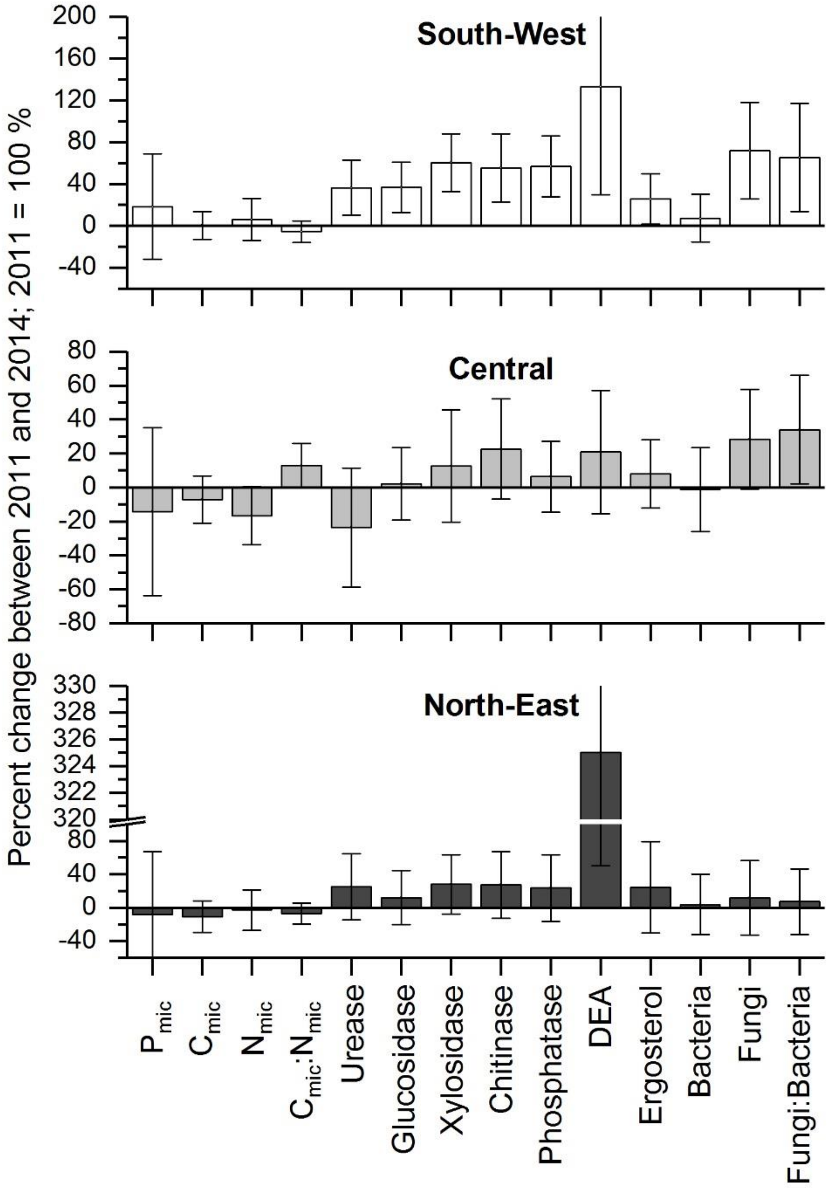
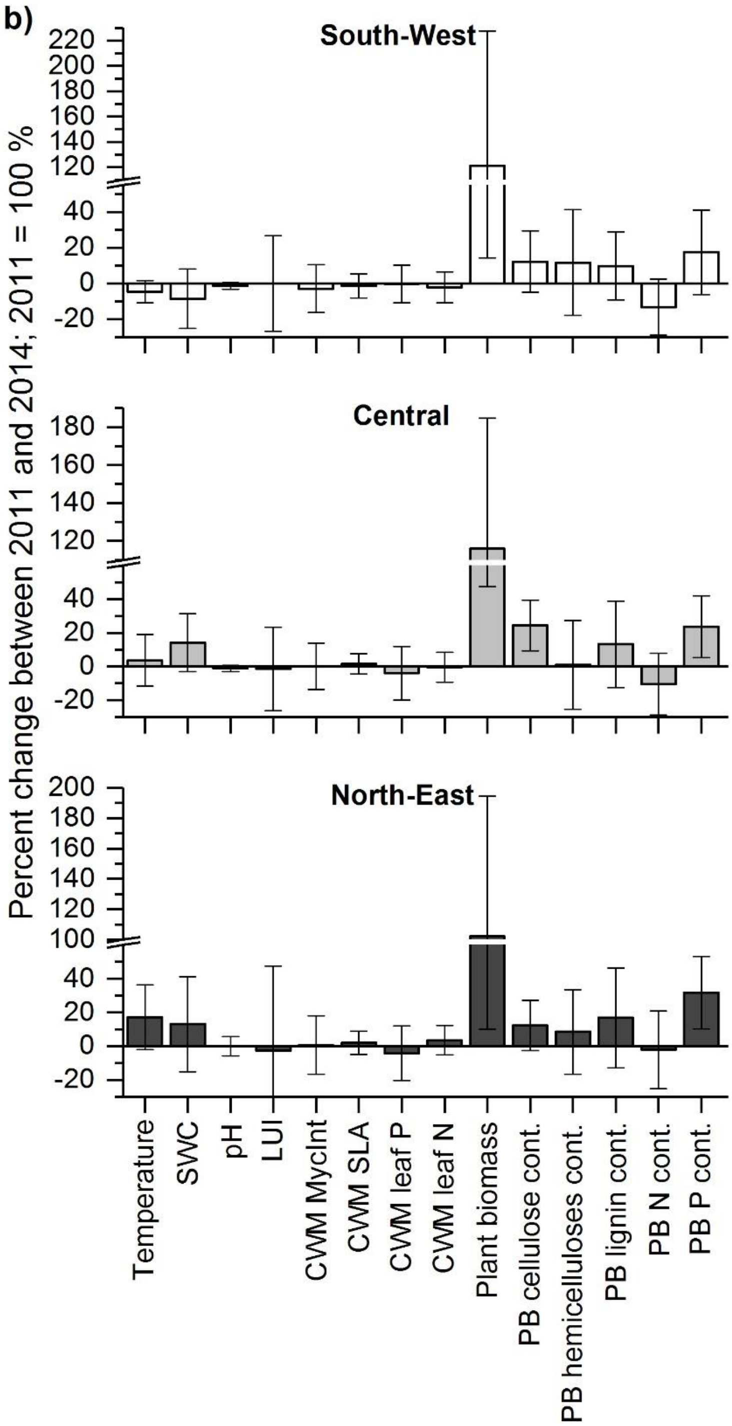


Figure 1: a) causal diagram of SEMs with one mediator variable (changes) for all regions, b) causal diagram of SEMs with both, historic and change values of mediator variable for all regions. LISREL notation is used. Driver I = LUI$_h$, Driver II = ΔLUI, mediator variables (I and II in order of appearance) are i) CWM leaf P$_h$ and ΔCWM leaf P, ii) CWM MycInt$_h$ and ΔCWM MycInt, iii) pH$_h$ and ΔpH, iv) Δplant biomass and v) Δlignin, response = endogenous soil microbial variable.

a)


South-West
Central
North-East
Percent change between 2011 and 2014; 2011 = 100 %
200
160
120
80
40
0
-40
80
60
40
20
0
-20
-40
-60
-80
330
328
326
324
322
320
80
40
0
-40
P_mic
C_mic
N_mic
C_mic:N_mic
Urease
Glucosidase
Xylosidase
Chitinase
Phosphatase
DEA
Ergosterol
Bacteria
Fungi
Fungi:Bacteria

b)
South-West
Central
North-East
Percent change between 2011 and 2014; 2011 = 100 %
220
200
180
160
140
120
100
40
20
0
-20
Temperature
SWC
pH
LUI
CWM MycInt
CWM SLA
CWM leaf P
CWM leaf N
Plant biomass
PB cellulose cont.
PB hemicelluloses cont.
PB lignin cont.
PB N cont.
PB P cont.

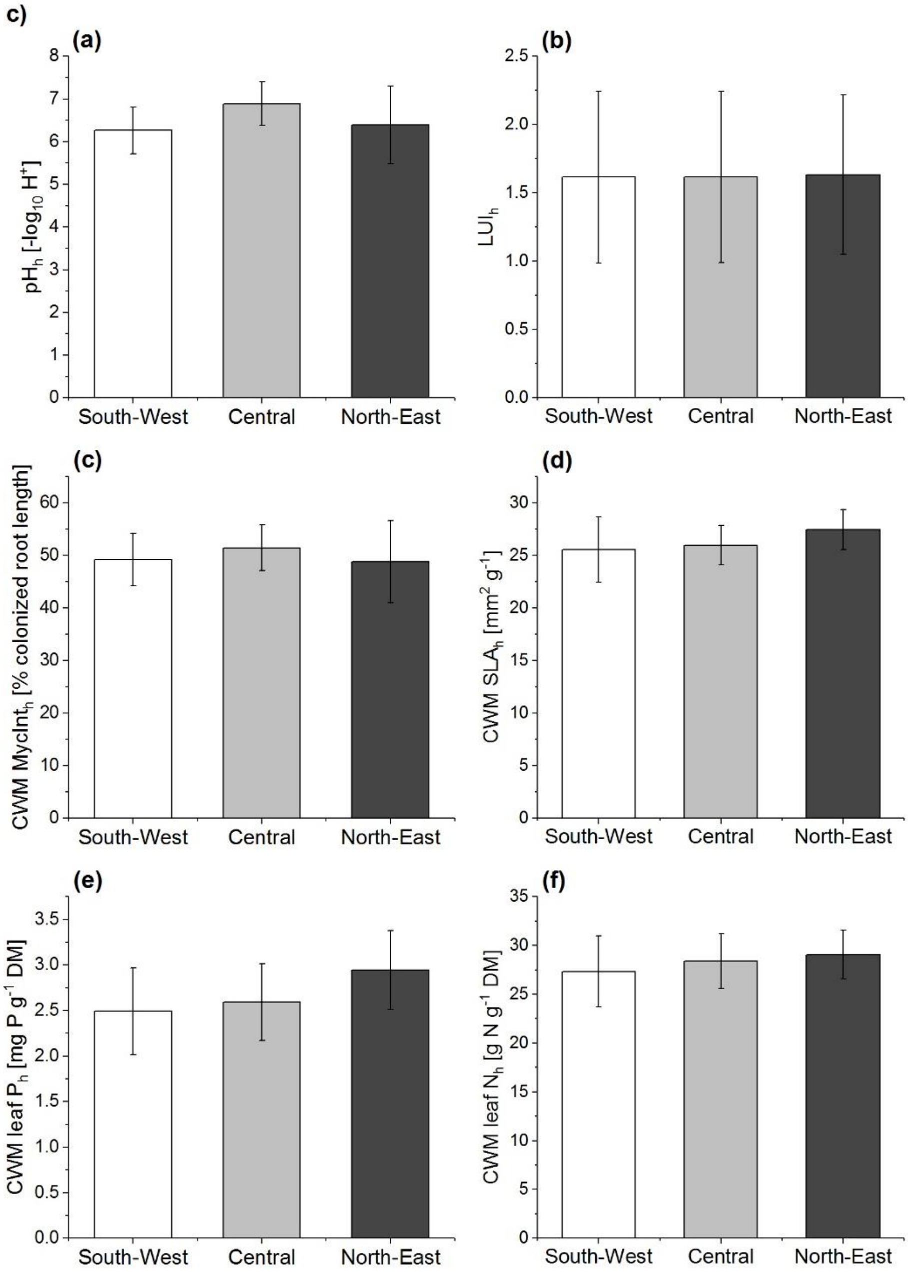


Figure 2: Mean regional changes in variables between 2011 and 2014 displayed as percent change of 2014 based on 2011 a) microbial soil properties, b) environmental, land management and plant variables, and c) historic mean values of explanatory variables for pH, LUI, CWM MycInt, CWM SLA, CWM leaf P and CWM leaf N (mean per region). Whiskers indicate standard deviation.

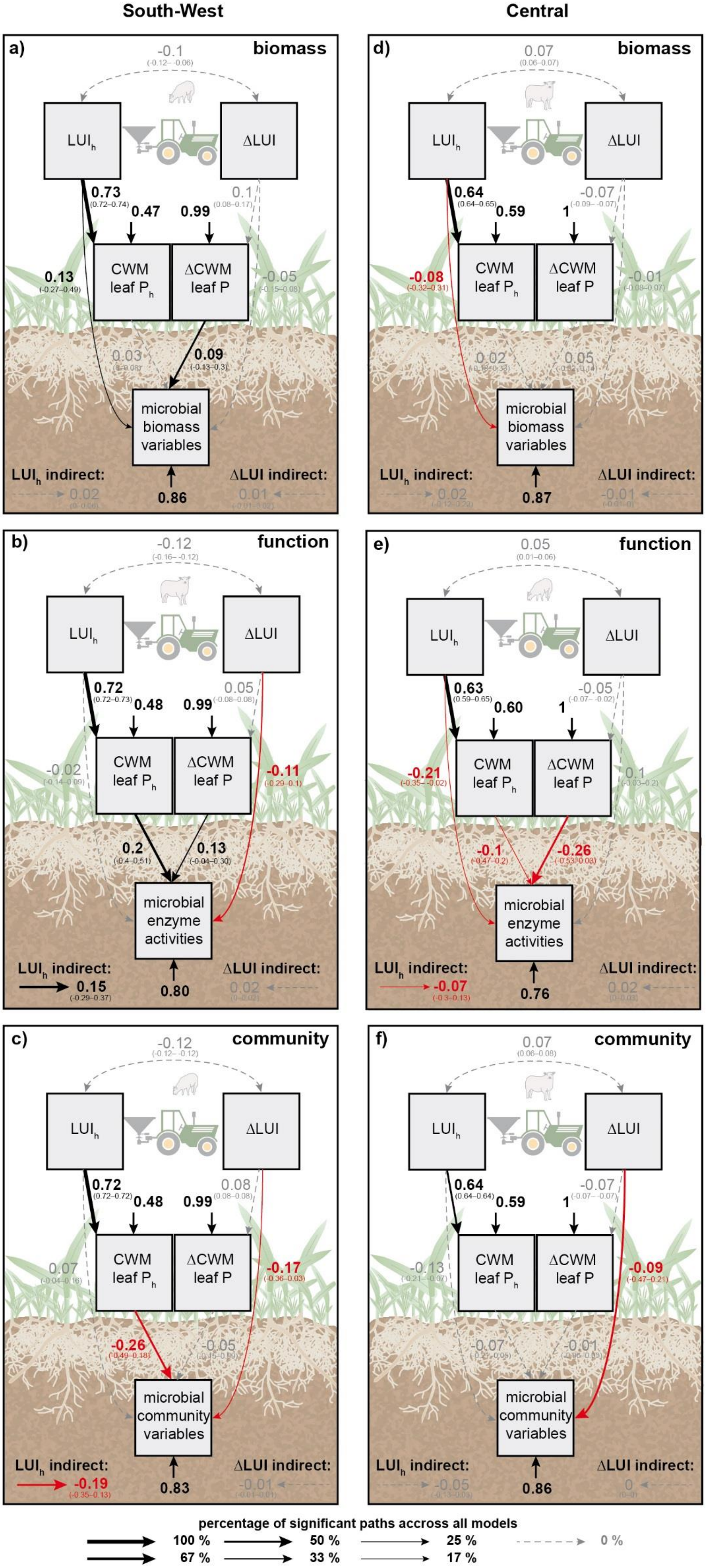
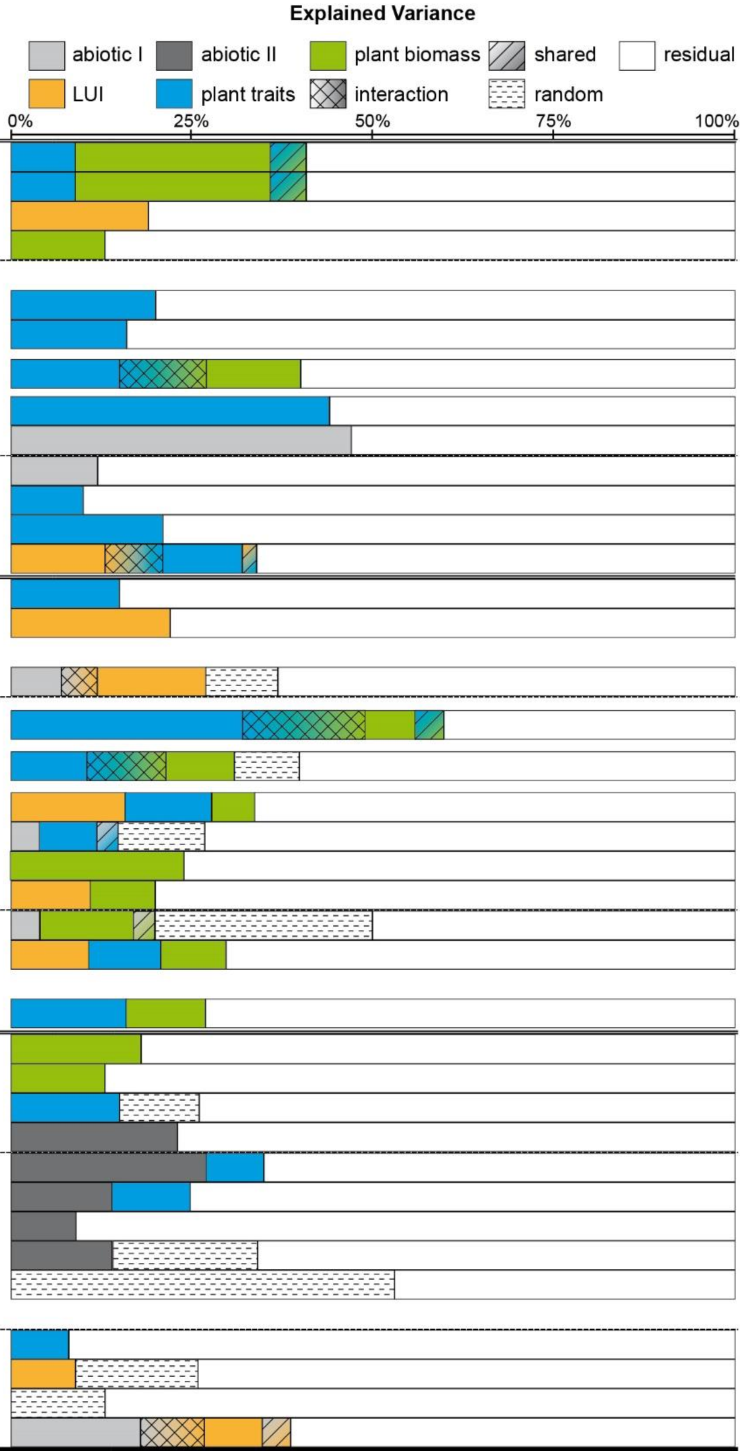

South-West
Central
a)
biomass
-0.1
(-0.12– -0.06)
LUI_h
ΔLUI
0.73
(0.72–0.74)
0.47
0.99
0.1
(0.08–0.17)
CWM leaf P_h
ΔCWM leaf P
0.13
(-0.27–0.49)
-0.05
(-0.15–0.08)
0.03
(0–0.08)
0.09
(-0.13–0.3)
microbial biomass variables
LUI_h indirect:
0.02
(0–0.06)
0.86
ΔLUI indirect:
0.01
(-0.01–0.02)
d)
biomass
0.07
(0.06–0.07)
LUI_h
ΔLUI
0.64
(0.64–0.65)
0.59
1
-0.07
(-0.09– -0.07)
CWM leaf P_h
ΔCWM leaf P
-0.08
(-0.32–0.31)
-0.01
(-0.08–0.07)
0.02
(-0.18–0.33)
0.05
(-0.02–0.14)
microbial biomass variables
LUI_h indirect:
0.02
(-0.12–0.22)
0.87
ΔLUI indirect:
-0.01
(-0.01–0)
b)
function
-0.12
(-0.16– -0.12)
LUI_h
ΔLUI
0.72
(0.72–0.73)
0.48
0.99
0.05
(-0.08–0.08)
CWM leaf P_h
ΔCWM leaf P
-0.02
(-0.14–0.09)
-0.11
(-0.29–0.1)
0.2
(-0.4–0.51)
0.13
(-0.04–0.30)
microbial enzyme activities
LUI_h indirect:
0.15
(-0.29–0.37)
0.80
ΔLUI indirect:
0.02
(0–0.02)
e)
function
0.05
(0.01–0.06)
LUI_h
ΔLUI
0.63
(0.59–0.65)
0.60
1
-0.05
(-0.07– -0.02)
CWM leaf P_h
ΔCWM leaf P
-0.21
(-0.35– -0.02)
0.1
(-0.03–0.2)
-0.1
(-0.47–0.2)
-0.26
(-0.53–0.03)
microbial enzyme activities
LUI_h indirect:
-0.07
(-0.3–0.13)
0.76
ΔLUI indirect:
0.02
(0–0.03)
c)
community
-0.12
(-0.12– -0.12)
LUI_h
ΔLUI
0.72
(0.72–0.72)
0.48
0.99
0.08
(0.08–0.08)
CWM leaf P_h
ΔCWM leaf P
0.07
(-0.04–0.16)
-0.17
(-0.36–0.03)
-0.26
(-0.49–0.18)
-0.05
(-0.15–0.09)
microbial community variables
LUI_h indirect:
-0.19
(-0.35–0.13)
0.83
ΔLUI indirect:
-0.01
(-0.01–0.01)
f)
community
0.07
(0.06–0.08)
LUI_h
ΔLUI
0.64
(0.64–0.64)
0.59
1
-0.07
(-0.07– -0.07)
CWM leaf P_h
ΔCWM leaf P
-0.13
(-0.21– -0.07)
-0.09
(-0.47–0.21)
-0.07
(-0.21–0.05)
-0.01
(-0.06–0.03)
microbial community variables
LUI_h indirect:
-0.05
(-0.13–0.03)
0.86
ΔLUI indirect:
0
(0–0)
percentage of significant paths accross all models
100 %
50 %
25 %
0 %
67 %
33 %
17 %

Figure 3: Summarized results of the SEMs of the South-West and Central regions. Figures a-f show the error weighted means of standardized estimates over all paths (with minimum and maximum estimates) for microbial variables: biomass (C_{mic}, N_{mic}, P_{mic}, C_{mic}:N_{mic} ratio), function (enzyme activities of glucosidase, xylosidase, chitinase, urease, DEA, phosphatase) and community composition (bacterial and fungal PLFA, fungi:bacteria ratio, ergosterol content). Path thickness relates to percentage of significant paths within each variable group. Dotted lines indicate paths that were never significant.

Tables

Table 1: Results of hierarchical regressions in South-West, Central and North-East Germany. Models are displayed in form of: $y_i = b_0 + b_1x_{1i} + b_2x_{2i} + \ldots + b_kx_{ki} + \varepsilon_i$. Bars indicate the percentage of unique variance explained by each level based on R^2; Δ = change, $_h$ = historic, n = number of observations.

Region	Category	Model	n
South-West	*biomass*	ΔC_{mic} = -29.29 + 112.5 * ΔCWM leaf P + 17.89 * Δplant biomass cellulose content	44
		ΔN_{mic} = 0.45 + 25.29 * ΔCWM leaf P + 4.1 * Δplant biomass cellulose content	44
		ΔP_{mic} = -12.45 + 12.16 * LUI_h	34
		$\Delta C_{mic}:N_{mic}$ ratio = -0.27 - 0.09 * Δplant biomass cellulose content	44
	function	Δglucosidase = no model fit	
		Δxylosidase = -110.65 + 10.45 * CWM SLA_h	44
		Δchitinase = 243.39 + 30.95 * ΔCWM SLA	41
		Δurease = 342.39 - 5.35 * CWM $MycInt_h$ + 504.22 * Δplant biomass N content - 9.16 * CWM $MycInt_h$: Δplant biomass N content	44
		ΔDEA = -0.31 + 0.67 * ΔCWM leaf P + 0.65 * CWM leaf P_h	44
		Δphosphatase = 4403 - 558.37 * pH_h	44
	community	Δbacteria = 3.02 - 15.52 * ΔTemp	44
		Δfungi = 16.12 - 0.4 * CWM SLA_h	44
		Δfungi:bacteria ratio = 0.14 - 0.04 * CWM leaf P_h	44
		Δergosterol = 8.85 - 18.99 ΔLUI - 2.24 * CWM leaf P_h + 6.28 ΔLUI:CWM leaf P_h	44
Central	*biomass*	ΔC_{mic} = 238.62 - 10.83 * CWM SLA_h + 8.13 * ΔCWM leaf N	48
		ΔN_{mic} = 4.86 - 13.26 * LUI_h	48
		ΔP_{mic} = -6.56	43
		$\Delta C_{mic}:N_{mic}$ ratio = -2.23 + 0.32 pH_h + 3.76 * LUI_h - 0.48 * pH_h:LUI_h	48
	function	Δglucosidase = -2827 + 100.78 * CWM SLA_h - 388.54 * ΔCWM leaf P + 25.65 * Δplant biomass - 0.94 * CWM SLA_h:Δplant biomass	48
		Δxylosidase = 16.71 + 99.42 * ΔCWM leaf P + 0.03 * Δplant biomass - 1.05 * ΔCWM leaf P:Δplant biomass	46
		Δchitinase = 207.82 - 85.2 LUI_h - 109.92 * ΔCWM leaf P + 25.3 * Δplant biomass lignin content	48
		Δurease = 75.45 + 10.16 * ΔTemp - 46.88 * CWM leaf P_h	43
		ΔDEA = -0.19 + 0.003 * Δplant biomass	48
		Δphosphatase = 144.22 - 129.23 * LUI_h + 0.79 * Δplant biomass	48
	community	Δbacteria = -71.64 + 8.66 * pH_h + 0.08 * Δplant biomass	48
		Δfungi = 0.84 - 1.82 * LUI_Δ + 0.27 ΔCWM leaf N + 0.01 * Δplant biomass	48
		Δfungi:bacteria ratio = no model fit	
		Δergosterol = 16.01 - 0.54 * CWM leaf N_h + 0.89 * Δplant biomass lignin content	45
North-East	*biomass*	ΔC_{mic} = -125.43 + 0.33 * Δplant biomass	49
		ΔN_{mic} = -13.27 + 0.06 * Δplant biomass	49
		ΔP_{mic} = -5.12 - 15.65 * ΔCWM leaf P	45
		$\Delta C_{mic}:N_{mic}$ ratio = -0.42 - 1.04 * ΔpH	49
	function	Δglucosidase = 194.69 + 729.2 * ΔpH - 17.46 * ΔCWM MycInt	49
		Δxylosidase = 78.3 + 98.46 * ΔpH - 3.88 * ΔCWM MycInt	49
		Δchitinase = 128.63 + 147.47 * ΔpH	49
		Δurease = 51.61 + 102.7 * ΔpH	49
		ΔDEA = 1.15	49
		Δphosphatase = no model fit	
	community	Δbacteria = -39.19 + 0.85 * CWM $MycInt_h$	49
		Δfungi = 0.46 + 0.44 * ΔLUI	49
		Δfungi:bacteria ratio = 0.01	49
		Δergosterol = 15.39 - 2.09 * pH_h + 14.58 ΔLUI - 1.96 * pH_h: ΔLUI	49



Appendix 1: Details on materials and methods

Plant functional trait shifts explain concurrent changes in the structure and function of grassland soil microbial communities

Boeddinghaus, R. S., Marhan, S., Berner, D., Boch, S., Fischer, M., Hölzel, N., Kattge, J., Klaus, V. H., Kleinebecker, T., Oelmann, Y., Prati, D., Schäfer, D., Schöning, I., Schrumpf, M., Sorkau, E., Kandeler, E. & Manning, P.

Land-use intensity

Land-use intensity varied on the sites over the years depending on farm management. The land-use intensity index (LUI) of Blüthgen et al. (2012) was used to assess mowing frequency as well as grazing and N-fertilization intensity standardized per region and is calculated by the formula:

$$LUI_i = \sqrt{\frac{F_i}{F_{mean,R}} + \frac{M_i}{M_{mean,R}} + \frac{G_i}{G_{mean,R}}}$$

Thereby *i* the site, *R* is the region, *F* is fertilization intensity in kg nitrogen ha^{-1} $year^{-1}$, *M* is number of cuts per year, and *G* is livestock density for grazing in livestock units days of grazing ha^{-1} a^{-1}, with 1 livestock unit = 500 kg animal life weight. Previous analyses have shown that the metric produces similar results when standardised by the means of all regions as the range of intensities with each is similar (Blüthgen et al., 2012, Allan et al., 2015).

Soil Microbial analyses

Microbial biomass measures

Microbial biomass carbon (C_{mic}) and nitrogen (N_{mic}) were measured using the chloroform-fumigation-extraction method (CFE) according to Vance, Brookes and Jenkinson (1987). Carbon and N were extracted from each, 24 h chloroform fumigated and non-fumigated, replicate (10 g) with 40 mL 0.5 M K_2SO_4 by shaking 30 minutes on a horizontal shaker at 150 rpm and subsequently centrifuging for 30 minutes at 4400 g. The supernatant was filtered, diluted by 1:4 and C and N concentrations in resulting extracts were measured on a TOC/TN analyzer (Multi N/C 2100S, Analytik Jena AG, Jena, Germany).

Microbial phosphorous (P_{mic}) was measured using a combination of methods by Kouno, Tuchiya and Ando (1995) and McLaughlin, Alston and Martin (1986). Conditioning of resin stripes was done using 0.5 M $NaHCO_3$ (pH = 8.5). Three aliquots of moist soil equalling 2 g of dry soil per sample were weighed into 50 mL polyethylene tubes and 30 mL distilled water (H_2O_{dest}) was added to each tube. One tube was non-fumigated (without aliquots (1) H_2O_{dest}), the second one was fumigated with 1 mL hexanol ((2) H_2O_{dest} and liquid hexanol) and at the third one 1 mL of 20 µg P mL^{-1} as dissolved KH_2PO_4 was added ((3) H_2O_{dest} and a P spike) to correct for P release during the fumigation. Soil samples were horizontally shaken for 16 hours with $NaHCO_3$ conducted resin membrane stripes. Afterwards, stripes were rinsed with H_2O_{dest} to remove adhering soil and transferred into fresh tubes. Afterwards, 30 mL 0.1 M sodium chloride/hydrochloric acid were added, and the resin stripes shaken for 2 hours to desorb P. To correct for sorption of P released during fumigation in the calculation of hexanol P, we used a sorption curve between non-fumigated and P spiked samples (Bünemann, 2008). We did not use a transformation factor for the calculated P_{hex} concentrations and used P_{mic} synonymously for P_{hex} in accordance with Oberson and Joner (2005) and Bünemann (2008).

Soil enzyme activities

Enzyme activities of beta-glucosidase (EC 3.2.1.21), beta-xylosidase (EC 3.2.1.37), N-acetyl-beta-glucosaminidase (EC 3.2.1.52), phosphatase (EC 3.1.3.1) and urease (EC 3.5.1.5) as well as denitrification enzyme activity (DEA) were measured in this study. The first four enzymes were determined using the method of Marx, Wood and Jarvis (2001) and fluorescent 4-methylumbelliferone substrates (4-MUF; Sigma- Aldrich, St. Louis, USA) together with a buffered solution of pH 6.1, as described in detail by Berner et al. (2011). Urease activity was measured photometrically according to Kandeler and Gerber (1988) as described in Schinner, Öhlinger, Kandeler and Margesin (1996).

Denitrification enzyme activity was measured after Keil et al. (2015) according to a method based on Smith and Tiedje (1979). Shortly, two replicates per soil sample with each 2 g fresh weight were weighed into three 118 mL flasks and 10 mL substrate solution (1.07 mM KNO_3 and 1 mM glucose) added. The bottles were closed air tight and oxygen was removed from the system by repeated evacuating and subsequently filling with N_2. 10 mL of N_2 were removed from the headspace and refilled with 10 mL of acetone-free acetylene. Bottles were incubated at 25 °C while shaking at 150 rpm and immediately, and after 30, 60 and 120 minutes 1 mL of the flask headspace was withdrawn with a gas-tight syringe and injected in pre-evacuated 5.9 mL exetainers (Labco scientific, UK) and 11 mL N_2 were added. Measurement of N_2O was done on a gas chromatograph (Agilent 7890 gas chromatograph equipped with an ECD detector, Agilent, Santa Clara, CA, USA). Potential N_2O release due to denitrification (ng N_2O g^{-1} dry soil h^{-1}) from soil was calculated from the linear regression of N_2O concentration against time.

Microbial community structure

Microbial community composition in terms of bacterial and fungal abundance was analysed using the phospholipid fatty acid composition of soils. Extraction was conducted following the protocol of Frostegard, Tunlid and Baath (1991). 2 g of soil were extracted with 9.2 mL of single-phase mixture (chloroform:methanol:citrate buffer (0.15 M, pH 4.0), 1:2:0.8, v:v:v) for 2 hours on a horizontal shaker (125 rpm) followed by centrifugation (2500 rpm, 10 minutes). The liquid phase was transferred into fresh centrifuge glasses and soil washed with 2.5 mL single-phase mixture, centrifuged (2500 rpm, 10 minutes) and the supernatant transferred as before. The supernatant solution was then mixed with 3.1 mL $CHCl_3$ and 3.1 mL citrate buffer on a horizontal shaker (275 rpm, 10 minutes) and centrifuged (2500 rpm, 10 minutes). 4 mL of the lower, lipid-containing phase was transferred into fresh test-tubes and the solvents evaporated on a heating plate at 37 °C under constant N_2 flow. The test-tubes with the dried lipid material were stored in a fridge over night at + 4 °C.

For the lipid fractionation, material was solved in 3 x 100 µL $CHCl_3$ and transferred on silica columns (Bond Elut-SI, 500 mg, 3 mL Agilent Technologies Inc. ,Santa Clara, USA) in a Baker System. After flushing out the neutral lipids (5 mL $CHCl_3$) and glycolipids (20 mL acetone) the columns were flushed with 5 mL methanol; this last fraction of polar lipids was collected in centrifuge test-tubes. Under a constant N_2 stream the methanol was evaporated on a heating plate at 40 °C until the samples were dried.

As a third step the alkaline methanolysis was performed after Dowling, Widdel and White (1986) to gain fatty acid methyl esters (FAME). The resulting organic phase, consistent of FAMEs from phospholipids and solvents, was evaporated under a constant N_2 stream at 40 °C. For measurement at the gas chromatograph (AutoSystem XL. PerkinElmer Inc., Massachusetts, USA) samples were solved in 100 µL isooctane and stored in GC vials at 4 °C until measurement. Following Ruess and Chamberlain (2010) the PLFA FAMEs a15:0, i15:0, i16:0, and i17:0 together with cy17:0 and cy19:0 as well as 16:1ω7 were used to represent soil bacteria, while PLFA FAME 18:2ω6,9 served as a fungal indicator. The fungal to bacteria ratio (F:B) was calculated.

Fungal biomass was also determined as ergosterol content of bio-membranes according to the modified approach of Djajakirana, Joergensen and Meyer (1996). Ergosterol was extracted from 2 g of soil with 25 mL ethanol during 30 minutes shaking on a horizontal shaker at 150 rpm. Solid particles were sedimented by centrifugation for 30 minutes at 4422 × g. 10 mL of the supernatant were dried at 50 °C in a vacuum rotary evaporator (Martin Christ, RVC 2-25, Osterode am Harz, Germany). Dried extracts were dissolved in 1 mL methanol and samples transferred into 2 mL brown glass HPLC vials via cellulose-acetate filters (0.45 µm; Sartorius Stedim Biotech GmbH, Gottingen, Germany). Ergosterol in samples was quantified by HPLC analysis (Beckmann Coulter, System Gold 125, Fullerton, USA) using a 250 mm × 4.6 mm Spherisorb ODS II 5 µm column with a mobile phase of pure methanol, a flow rate of 1 mL minute^{-1} and a detection wavelength of 282 nm (Beckmann Coulter, System Gold 166 UV-detector, Fullerton, USA). Pure ergosterol (Sigma–Aldrich, St. Louis, USA) for calibration was dissolved in methanol and diluted to give final concentrations of 0.0, 0.1, 0.2, 0.5, 1.0, 2.0, 5 and 10 µg ergosterol mL^{-1}.

Abiotic soil analyses

Nitrate and ammonium were extracted from 10 g soil with 0.5 M K_2SO_4 solution (1:4, g soil:mL solution) following the isonorm protocol DIN ISO 14256-2 (2006) and measured with an AutoAnalyzer 3 (Bran & Luebbe, Norderstedt, Germany). Nitrate was measured at 550 nm wavelength and ammonium at 660 nm. To determine extractable organic carbon (EOC) and extractable nitrogen (EN) the extracts for analysing mineral nitrogen were diluted 1:4 and measured using a TOC/TN analyser (Multi N/C 2100S, Analytik Jena AG, Jena, Germany). Total C (C_{org}) and total N (N_t) were measured by dry combustion using an elemental analyser (VarioMax, Elementar Analysensysteme GmbH, Hanau, Germany). Inorganic C was determined after removal of organic C at a temperature of 450 °C for 16 h. The difference between total and inorganic C equals the organic C. Bulk density was calculated as g dry soil, excluding stones, per cubic centimetre.

Plant data

Plant traits

Single plant species trait values from the TRY database (Kattge et al., 2011) were obtained by averaging the data by author. This way, disproportionate contributions of one author to a single species was accounted for. Where trait data was not available for single species recorded at the field sites, the CWM was calculated using only known species. This only occurred for very few species which accounted overall for 0.05% of total plot coverage and therefore did not affect the overall results.

Reference list for request 250 from TRY database:

Dataset	Reference
Jasper Ridge Californian Woody Plants Database	Ackerly, D. D. and W. K. Cornwell. 2007. A trait-based approach to community assembly: partitioning of species trait values into within- and among-community components. Ecology Letters 10:135-145.
Plant Physiology Database	Atkin, O. K., M. H. M. Westbeek, M. L. Cambridge, H. Lambers, and T. L. Pons. 1997. Leaf respiration in light and darkness - A comparison of slow- and fast-growing Poa species. Plant Physiology 113:961-965.
Plant Physiology Database	Atkin, O. K., M. Schortemeyer, N. McFarlane, and J. R. Evans. 1999. The response of fast- and slow-growing Acacia species to elevated atmospheric CO2: an analysis of the underlying components of relative growth rate. Oecologia 120:544-554.

Dataset	Reference
The RAINFOR Plant Trait Database	Baker, T. R., O.L. Phillips, W.F. Laurance, N.C.A. Pitman, S. Almeida, L. Arroyo, A. DiFiore, T. Erwin, N. Higuchi, T.J. Killeen, S.G. Laurance, H. Nascimento, A. Monteagudo, D.A. Neill, J.N.M. Silva, Y. Malhi, G. Lopez Gonzalez, J. Peacock, C.A. Quesada, S. L. Lewis, and J. Lloyd. 2009. Do species traits determine patterns of wood production in Amazonian forests? Biogeosciences 6:297-307.
Wetland Dunes Database	Bakker, C., J. Rodenburg, and P. Bodegom. 2005. Effects of Ca- and Fe-rich seepage on P availability and plant performance in calcareous dune soils. Plant and Soil 275:111-122.
Wetland Dunes Database	Bakker, C., P. M. Van Bodegom, H. J. M. Nelissen, W. H. O. Ernst, and R. Aerts. 2006. Plant responses to rising water tables and nutrient management in calcareous dune slacks. Plant Ecology 185:19-28.
Plant Physiology Database	Campbell, C., L. Atkinson, J. Zaragoza-Castells, M. Lundmark, O. Atkin, and V. Hurry. 2007. Acclimation of photosynthesis and respiration is asynchronous in response to changes in temperature regardless of plant functional group. New Phytologist 176:375-389.
Sheffield & Spain Woody Database	Castro-Diez, P., J. P. Puyravaud, and J. H. C. Cornelissen. 2000. Leaf structure and anatomy as related to leaf mass per area variation in seedlings of a wide range of woody plant species and types. Oecologia 124:476-486.
Sheffield & Spain Woody Database	Castro-Diez, P., J. P. Puyravaud, J. H. C. Cornelissen, and P. Villar-Salvador. 1998. Stem anatomy and relative growth rate in seedlings of a wide range of woody plant species and types. Oecologia 116:57-66.
Global Wood Density Database	Chave, J., D. Coomes, S. Jansen, S. L. Lewis, N. G. Swenson, and A. E. Zanne. 2009. Towards a world wide wood economics spectrum. Ecology Letters 12:351-366.
Sheffield Database	Cornelissen, J. H. C. 1996. An experimental comparison of leaf decomposition rates in a wide range of temperate plant species and types. Journal of Ecology 84:573-582.
Sheffield Database	Cornelissen, J. H. C., B. Cerabolini, P. Castro-Diez, P. Villar-Salvador, G. Montserrat-Marti, J. P. Puyravaud, M. Maestro, M. J. A. Werger, and R. Aerts. 2003. Functional traits of woody plants: correspondence of species rankings between field adults and laboratory-grown seedlings? Journal of Vegetation Science 14:311-322.
Sheffield & Spain Woody Database	Cornelissen, J. H. C., B. Cerabolini, P. Castro-Diez, P. Villar-Salvador, G. Montserrat-Marti, J. P. Puyravaud, M. Maestro, M. J. A. Werger, and R. Aerts. 2003. Functional traits of woody plants: correspondence of species rankings between field adults and laboratory-grown seedlings? Journal of Vegetation Science 14:311-322.
Abisko & Sheffield Database	Cornelissen, J. H. C., H. M. Quested, D. Gwynn-Jones, R. S. P. Van Logtestijn, M. A. H. De Beus, A. Kondratchuk, T. V. Callaghan, and R. Aerts. 2004. Leaf digestibility and litter decomposability are related in a wide range of subarctic plant species and types. Functional Ecology 18:779-786.
Abisko & Sheffield Database	Cornelissen, J. H. C., M. J. A. Werger, P. CastroDiez, J. W. A. vanRheenen, and A. P. Rowland. 1997. Foliar nutrients in relation to growth, allocation and leaf traits in seedlings of a wide range of woody plant species and types. Oecologia 111:460-469.
Sheffield Database	Cornelissen, J. H. C., N. Perez-Harguindeguy, S. Diaz, J. P. Grime, B. Marzano, M. Cabido, F. Vendramini, and B. Cerabolini. 1999. Leaf structure and defence control litter decomposition rate across species and life forms in regional floras on two continents. New Phytologist 143:191-200.
Abisko & Sheffield Database	Cornelissen, J. H. C., P. C. Diez, and R. Hunt. 1996. Seedling growth, allocation and leaf attributes in a wide range of woody plant species and types. Journal of Ecology 84:755-765.
Sheffield Database	Cornelissen, J. H. C., P. C. Diez, and R. Hunt. 1996. Seedling growth, allocation and leaf attributes in a wide range of woody plant species and types. Journal of Ecology 84:755-765.
Sheffield Database	Cornelissen, J. H. C., R. Aerts, B. Cerabolini, M. J. A. Werger, and M. G. A. van der Heijden. 2001. Carbon cycling traits of plant species are linked with mycorrhizal strategy. Oecologia 129:611-619.
Sheffield & Spain Woody Database	Cornelissen, J.H.C. 1999. A triangular relationship between leaf size and seed size among woody species: allometry, ontogeny, ecology and taxonomy. Oecologia 118: 248-255.
Jasper Ridge Californian Woody Plants Database	Cornwell, W. K. and D. D. Ackerly. 2009. Community assembly and shifts in plant trait distributions across an environmental gradient in coastal California. Ecological Monographs 79:109-126.
Jasper Ridge Californian Woody Plants Database	Cornwell, W. K., D. W. Schwilk, and D. D. Ackerly. 2006. A trait-based test for habitat filtering: Convex hull volume. Ecology 87:1465-1471.
ArtDeco Database	Cornwell, W. K., J. H. C. Cornelissen, K. Amatangelo, E. Dorrepaal, V. T. Eviner, O. Godoy, S. E. Hobbie, B. Hoorens, H. Kurokawa, N. Pérez-Harguindeguy, H. M. Quested, L. S.

Dataset	Reference
	Santiago, D. A. Wardle, I. J. Wright, R. Aerts, S. D. Allison, P. van Bodegom, V. Brovkin, A. Chatain, T. V. Callaghan, S. Díaz, E. Garnier, D. E. Gurvich, E. Kazakou, J. A. Klein, J. Read, P. B. Reich, N. A. Soudzilovskaia, M. V. Vaieretti, and M. Westoby. 2008. Plant species traits are the predominant control on litter decomposition rates within biomes worldwide. Ecology Letters 11:1065-1071.
Global 15N Database	Craine, J. M., A. J. Elmore, M. P. M. Aidar, M. Bustamante, T. E. Dawson, E. A. Hobbie, A. Kahmen, M. C. Mack, K. K. McLauchlan, A. Michelsen, G. B. Nardoto, L. H. Pardo, J. Penuelas, P. B. Reich, E. A. G. Schuur, W. D. Stock, P. H. Templer, R. A. Virginia, J. M. Welker, and I. J. Wright. 2009. Global patterns of foliar nitrogen isotopes and their relationships with climate, mycorrhizal fungi, foliar nutrient concentrations, and nitrogen availability. New Phytologist 183:980-992.
Roots Of the World (ROW) Database	Craine, J. M., W. G. Lee, W. J. Bond, R. J. Williams, and L. C. Johnson. 2005. Environmental constraints on a global relationship among leaf and root traits of grasses. Ecology 86:12-19.
Sheffield Database	Díaz, S., J. G. Hodgson, K. Thompson, M. Cabido, J. H. C. Cornelissen, A. Jalili, G. Montserrat-Martí, J. P. Grime, F. Zarrinkamar, Y. Asri, S. R. Band, S. Basconcelo, P. Castro-Díez, G. Funes, B. Hamzehee, M. Khoshnevi, N. Pérez-Harguindeguy, M. C. Pérez-Rontomé, F. A. Shirvany, F. Vendramini, S. Yazdani, R. Abbas-Azimi, A. Bogaard, S. Boustani, M. Charles, M. Dehghan, L. de Torres-Espuny, V. Falczuk, J. Guerrero-Campo, A. Hynd, G. Jones, E. Kowsary, F. Kazemi-Saeed, M. Maestro-Martínez, A. Romo-Díez, S. Shaw, B. Siavash, P. Villar-Salvador, and M. R. Zak. 2004. The plant traits that drive ecosystems: Evidence from three continents. Journal of Vegetation Science 15:295-304.
The DIRECT Plant Trait Database	Everwand G, Fry, EL, Eggers T, Manning P (2014) Seasonal variation in the relationship between plant traits and grassland carbon and water fluxes. Ecosystems 17, 1095-1108
Fonseca/Wright New South Wales Database	Fonseca, C. R., J. M. Overton, B. Collins, and M. Westoby. 2000. Shifts in trait-combinations along rainfall and phosphorus gradients. Journal of Ecology 88:964-977.
The VISTA Plant Trait Database	Fortunel, C., E. Garnier, R. Joffre, E. Kazakou, H. Quested, K. Grigulis, S. Lavorel, P. Ansquer, H. Castro, P. Cruz, J. Dolezal, O. Eriksson, H. Freitas, C. Golodets, C. Jouany, J. Kigel, M. Kleyer, V. Lehsten, J. Leps, T. Meier, R. Pakeman, M. Papadimitriou, V. P. Papanastasis, F. Quetier, M. Robson, M. Sternberg, J. P. Theau, A. Thebault, and M. Zarovali. 2009. Leaf traits capture the effects of land use changes and climate on litter decomposability of grasslands across Europe. Ecology 90:598-611.
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Categorical Plant Traits Database	unpub.

Dataset	Reference
Overton/Wright New Zealand Database	unpub.
Leaf Physiology Database	unpub.
Tundra Plant Traits Database	unpub.
Causasus Plant Traits Database	unpub.
Ukraine Wetlands Plant Traits Database	unpub.
New South Wales Plant Traits Database	unpub.
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Plant biomass properties

Aboveground community biomass was sampled in May 2011 and 2014 by cutting the vegetation at a height of 2–3 cm in four 0.5 × 0.5 m subplots in close proximity to the vegetation quadrat. In meadows, we sampled plant biomass at the same time as the first hay harvest by the farmer. In pastures and mown pastures, we temporarily fenced our subplots to ensure that the vegetation had not been grazed before plant biomass sampling. The biomass was dried at 80 °C for 48 hr, weighed, and ground to fine powder using cyclone mill (Cyclotec 1093, Foss, Höganäs, Sweden). Samples were analysed for the percent neutral detergent fibre (NDF), acid detergent fibre (ADF) and acid detergent lignin (ADL, lignin), as well as P and N content using near-infrared spectroscopy (NIRS). The concentrations were derived from previously established calibration models by recording a specific reflectance spectrum of each sample from 1250 to 2350 nm at intervals of 1 nm (algorithmically averaged over 24 measurements). For details see Klaus et al. (2016) and Kleinebecker, Klaus and Hölzel (2011). From these measures, cellulose (= ADF – ADL), hemicelluloses (= NDF – ADF) and the lignin to N ratio were calculated according to Kirchgeßner (2014).

Statistical analyses

Statistical modelling of changes in soil properties

In preliminary hierarchical regression model analyses we found that several variables were not significantly related to any soil microbial community and function variables. These were: measures of plant species richness, functional diversity (Rao’s Q index), a composite measure of plant traits representing the fast-slow spectrum based upon the first axis scores of a principal component analysis of CWM SLA, CWM leaf P and CWM leaf N, plant functional group identity (abundance of legumes, grasses and forbs) and lignin:N ratio of plant biomass. These variables were omitted from the final modelling procedure to reduce its complexity.

Structural equation models

We tested two estimators, ML (maximum likelihood estimation) and the more robust towards non-normal distribution and heteroscedasticity estimator MLM (maximum likelihood estimation with robust standard errors and a Satorra-Bentler scaled test statistic (Rosseel, 2012)), on a subset of variables for each region from all three categories – biomass, enzyme activities and community composition (C_{mic}, N_{mic}, C_{mic}:N_{mic}, glucosidase, phosphatase, urease, bacterial PLFA and fungal PLFA). The two estimators (ML and MLM) gave the same outcome – CWM leaf P was the best mediator variable in the South-West and Central regions and unfortunately the covariance matrices of SEMs in the North-East regions differed significantly from the data for both estimators.

There were some small differences in the exact values calculated with the two estimators: comparing the results obtained by MLM to those of ML yielded an increase in the number of significant paths by <1% (both for standardized and unstandardized *p*-values) and, on average, standard errors were 2.5% higher for unstandardized and 2.7% lower for standardized errors, while z-values were higher by 2.5% (unstandardized) and 6.1% (standardized) when using MLM. Unstandardized regression coefficients and standardized correlation coefficients were identical in 100% of cases and R^2 values of the models in 99.7% of cases. As the results did not essentially differ from each other, we chose the default ML estimator for our SEMs.

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Appendix 2
R-Code example for hierarchical regression modelling and structural equation models to the manuscript entitled "Plant functional trait shifts explain concurrent changes in the structure and function of grassland soil microbial communities"

Boeddinghaus, R. S., Marhan, S., Berner, D., Boch, S., Fischer, M., Hölzel, N., Kattge, J., Klaus, V. H., Kleinebecker, T., Oelmann, Y., Prati, D., Schäfer, D., Schöning, I., Schrumpf, M., Sorkau, E., Kandeler, E. and Manning, P.

March 22, 2019

Here, we present the R-code for the data analyses of the manuscript entitled "Plant functional trait shifts explain concurrent changes in the structure and function of grassland soil microbial communities". It contains the data analyses of fungal PLFA by hierarchical regression modelling and structural equation modelling as example for the code used on all other microbial variables encompassed in this manuscript.

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1 Hierarchical regression modelling

The hierarchical set up of the model contains five levels as follows: `lm(soil property change∼environment + landmanagement + plant functional traits + plant biomass properties)`. The level contents are displayed in Table 1 with Δ= change, $_{\mathrm{bv}}$ = background value, and $_{\mathrm{h}}$ = historic:

Table 1: Overview on hierarchical levels in the modelling process

Level	**overall description**	**fixed effects**
Level 1	environmental factors	Δtemperature, Δsoil water content, $\mathrm{pH}_{\mathrm{bv}}$
Level 2	land management	ΔLUI, $\mathrm{LUI}_{\mathrm{h}}$
Level 3	pH change	ΔpH
Level 4	plant functional traits	Δmycorrhizal intensity, mycorrhizal $\mathrm{intensity}_{\mathrm{h}}$, ΔSLA, $\mathrm{SLA}_{\mathrm{h}}$, Δleaf P, leaf P_{h}, Δleaf N, leaf N_{h}
Level 5	plant biomass properties	Δplant biomass, Δplant biomass cellulose content, Δplant biomass hemicellulose content, Δplant biomass lignin content, Δplant biomass P content, Δplant biomass N content

We start with a null model and add the individual fixed effects of the 1^{st} level, each time testing for AIC. After all fixed effect variables of that level have been tested individually, those which improved AIC by more than 2 were combined in one model and the `step()` function used to chose the best combination of fixed effects based on AIC. Afterwards, each of the fixed effects was tested for significance (p-values <0.05). The significant fixed effects were kept in the model and first order interactions between all fixed effects were tested for significance. All significant fixed effects and interactions after the the first level represented the null model for the next level. This procedure was used throuhgout all levels. It could happen during the process, that variables added later on replaced others which were added before, but became insignificant after addition of a new variable. Only significant variables and interactions were kept in the final model.

As the gradient length (range of values) within one exploratory for the fixed effects is not long, we do not expect a polynomial curve structure and therefore use linear variables without, e.g., quadratic terms.

Analysis procedure:

1. set up basic model and test spatial autocorrelation structures
2. test if correlation structures can be replaced by random effects, i.e. PlotID and soil type
3. test if random structure is needed at all
4. choose null model based on previous tests
5. select fixed effects (see above)
6. set up final full model and display its results

Spatial correlation structure:

All plots have latitude and longitude data, as well as the respective easting and northing assigned. Some of the variance in the data might be explained by the different spatial locations of the various plots. Therefore, we identify the spatial autocorrelation structure for our models. As metric system we use the default `euclidean` distance for the root sum-of-squares of distances.

There are several spatial correlation structures, which are tested for:

- exponential spatial correlation (corExp)
- Gaussian spatial correlation (corGaus)
- spherical spatial correlation (corSpher)
- linear spatial correlation (corLin)
- Rational quadratics spatial correlation (corRatio)

1.1 Hierarchical regressions for fungal PLFA

Load data:

```
regression_data_all <- read.table(file = "regression_data_all_2017-11_R.txt", header = T)

summary(regression_data_all)

##      PlotID    Exploratory   LUI_change         Graz_change       Fert_change       Mow_change
##  AEG01  :  1   ALB:50      Min.   :-2.016265   Min.   :-3.8989   Min.   :-7.959   Min.   :-2.2300
##  AEG02  :  1   HAI:50      1st Qu.:-0.289367   1st Qu.:-0.2934   1st Qu.: 0.000   1st Qu.:-0.1023
##  AEG03  :  1   SCH:50      Median :-0.006556   Median : 0.0000   Median : 0.000   Median : 0.0000
##  AEG04  :  1               Mean   :-0.021365   Mean   : 0.0000   Mean   : 0.000   Mean   : 0.0000
##  AEG05  :  1               3rd Qu.: 0.258984   3rd Qu.: 0.3584   3rd Qu.: 0.000   3rd Qu.: 0.0000
##  AEG06  :  1               Max.   : 2.721237   Max.   : 6.5584   Max.   :13.651   Max.   : 2.3810
##  (Other):144
##     CN_ratio          pH_change             Pmic              Cmic              Nmic
##  Min.   :-0.89464   Min.   :-1.63500   Min.   :-44.053   Min.   :-362.66   Min.   :-68.296
##  1st Qu.:-0.21299   1st Qu.:-0.15500   1st Qu.:-11.905   1st Qu.: -87.72   1st Qu.:-17.914
##  Median :-0.06519   Median :-0.08500   Median : -5.153   Median : -41.55   Median : -5.407
##  Mean   :-0.09290   Mean   :-0.05487   Mean   : -0.457   Mean   : -35.50   Mean   : -4.272
##  3rd Qu.: 0.05864   3rd Qu.: 0.00375   3rd Qu.:  8.523   3rd Qu.:  23.98   3rd Qu.:  8.150
##  Max.   : 1.54483   Max.   : 1.39000   Max.   : 66.594   Max.   : 224.35   Max.   : 62.877
##                                        NA's   :20
##  RatioCmic_Nmic         Urease         Glucosidase        Xylosidase        Chitinase
##  Min.   :-2.88932   Min.   :-224.06   Min.   :-990.61   Min.   :-251.36   Min.   :-291.36
##  1st Qu.:-0.58188   1st Qu.: -18.34   1st Qu.: -11.31   1st Qu.:  20.18   1st Qu.:  43.04
##  Median :-0.09740   Median :  29.16   Median : 195.68   Median :  84.19   Median : 119.93
##  Mean   :-0.01498   Mean   :  30.24   Mean   : 241.78   Mean   :  88.66   Mean   : 151.51
##  3rd Qu.: 0.56108   3rd Qu.:  75.18   3rd Qu.: 508.15   3rd Qu.: 150.85   3rd Qu.: 260.73
##  Max.   : 2.71386   Max.   : 347.94   Max.   :1434.12   Max.   : 386.74   Max.   : 711.18
##                     NA's   :5                           NA's   :2         NA's   :3
##   Phosphatase           DEA            Ergosterol         gram_pos           gram_neg
##  Min.   :-1043.8   Min.   :-1.3181   Min.   :-7.0878   Min.   :-47.8009   Min.   :-10.1362
##  1st Qu.:  111.6   1st Qu.: 0.3401   1st Qu.: 0.4036   1st Qu.: -8.6523   1st Qu.: -0.4207
##  Median :  353.9   Median : 0.7217   Median : 2.0094   Median :  0.6145   Median :  1.5282
##  Mean   :  497.5   Mean   : 1.2429   Mean   : 2.2251   Mean   :  0.3761   Mean   :  1.9177
##  3rd Qu.:  783.2   3rd Qu.: 1.8726   3rd Qu.: 3.6506   3rd Qu.:  7.2329   3rd Qu.:  4.0992
##  Max.   : 5400.0   Max.   : 7.7424   Max.   :24.6228   Max.   : 69.0361   Max.   : 20.1580
##                                      NA's   :3
##     bactotal           fungi           fungi_bac         invertebrates      Summe_mikro
##  Min.   :-82.709   Min.   :-4.4981   Min.   :-0.042755   Min.   :-0.9979   Min.   :-63.58
##  1st Qu.:-10.223   1st Qu.: 0.4738   1st Qu.: 0.002091   1st Qu.:-0.1466   1st Qu.: 33.41
##  Median :  3.725   Median : 1.7975   Median : 0.021682   Median : 0.2663   Median : 64.47
##  Mean   :  3.429   Mean   : 2.7771   Mean   : 0.028871   Mean   : 0.4701   Mean   : 73.18
##  3rd Qu.: 14.580   3rd Qu.: 4.8302   3rd Qu.: 0.051347   3rd Qu.: 1.0906   3rd Qu.:101.92
##  Max.   : 95.554   Max.   :15.3757   Max.   : 0.150446   Max.   : 3.0566   Max.   :291.08
##
##   RatioCmic_Ct      nbsp_change      RaoQ_change         CWM_Myc_int_change CWM_SLA_change
##  Min.   :-4.7284   Min.   :-6.000   Min.   :-0.0085986   Min.   :-29.4599   Min.   :-5.0499
##  1st Qu.:-0.9559   1st Qu.: 1.000   1st Qu.:-0.0004898   1st Qu.: -3.4171   1st Qu.:-0.8480
##  Median : 0.1799   Median : 3.000   Median : 0.0014843   Median :  0.1407   Median : 0.2078
##  Mean   : 0.1594   Mean   : 3.331   Mean   : 0.0018352   Mean   : -0.3410   Mean   : 0.1964
##  3rd Qu.: 1.3024   3rd Qu.: 6.000   3rd Qu.: 0.0036900   3rd Qu.:  4.4686   3rd Qu.: 1.3105
##  Max.   : 6.6702   Max.   :21.000   Max.   : 0.0138481   Max.   : 15.9860   Max.   : 5.0329
##  NA's   :1         NA's   :2        NA's   :2            NA's   :2          NA's   :2
##  CWM_leafP_change   CWM_leafN_change  CWM_LDMC_change       no_grasses       no_legumes
##  Min.   :-1.33210   Min.   :-7.7193   Min.   :-0.093339   Min.   :-6.000   Min.   :-3.0000
##  1st Qu.:-0.31316   1st Qu.:-1.3484   1st Qu.:-0.026612   1st Qu.:-1.000   1st Qu.:-1.0000
##  Median :-0.04561   Median : 0.2613   Median :-0.010017   Median : 1.000   Median : 0.0000
##  Mean   :-0.07882   Mean   : 0.1075   Mean   :-0.008479   Mean   : 0.604   Mean   : 0.1342
##  3rd Qu.: 0.12778   3rd Qu.: 1.8732   3rd Qu.: 0.014812   3rd Qu.: 2.000   3rd Qu.: 1.0000
##  Max.   : 1.81179   Max.   : 7.9321   Max.   : 0.110865   Max.   : 8.000   Max.   : 4.0000
##  NA's   :2          NA's   :2         NA's   :2           NA's   :1        NA's   :1
##     no_herbs       Plant_Biomass      Cellulose       Hemicellulosen        Lignin
##  Min.   :-15.000   Min.   :-81.55   Min.   :-3.5370   Min.   :-16.590   Min.   :-2.5870
##  1st Qu.: -1.000   1st Qu.: 73.20   1st Qu.: 0.8545   1st Qu.: -2.144   1st Qu.:-0.2475
##  Median :  2.000   Median :154.60   Median : 2.2070   Median :  1.383   Median : 0.6140
##  Mean   :  1.342   Mean   :167.34   Mean   : 2.6439   Mean   :  1.575   Mean   : 0.6297
##  3rd Qu.:  3.000   3rd Qu.:238.85   3rd Qu.: 4.5150   3rd Qu.:  5.697   3rd Qu.: 1.4410
##  Max.   : 10.000   Max.   :611.85   Max.   :10.0720   Max.   : 16.381   Max.   : 3.9210
##  NA's   :1         NA's   :1        NA's   :3         NA's   :3         NA's   :3
##      Pfl_N            Pfl_P          Lignin_N_ratio     Fast_Slow_Gradient_change nbsp_historic
##  Min.   :-1.260   Min.   :-0.07700   Min.   :-1.49778   Min.   :-3.70365          Min.   :13.00
##  1st Qu.:-0.444   1st Qu.: 0.02300   1st Qu.: 0.08135   1st Qu.:-0.88178          1st Qu.:19.25
##  Median :-0.188   Median : 0.05900   Median : 0.47539   Median :-0.06923          Median :24.25
##  Mean   :-0.185   Mean   : 0.05397   Mean   : 0.55457   Mean   : 0.00000          Mean   :26.53
##  3rd Qu.: 0.131   3rd Qu.: 0.08600   3rd Qu.: 0.91583   3rd Qu.: 0.82979          3rd Qu.:30.25
##  Max.   : 1.391   Max.   : 0.18500   Max.   : 2.62676   Max.   : 4.35581          Max.   :61.75
##  NA's   :3        NA's   :3          NA's   :3          NA's   :2
```

```
##  RaoQ_historic      CWM_Myc_int_historic CWM_SLA_historic CWM_leafP_historic CWM_leafN_historic
##  Min.   :0.008352   Min.   :27.45        Min.   :19.91    Min.   :1.548      Min.   :19.03     
##  1st Qu.:0.015276   1st Qu.:46.92        1st Qu.:25.36    1st Qu.:2.427      1st Qu.:26.74     
##  Median :0.016924   Median :50.53        Median :26.67    Median :2.704      Median :28.74     
##  Mean   :0.017109   Mean   :49.79        Mean   :26.32    Mean   :2.675      Mean   :28.25     
##  3rd Qu.:0.018595   3rd Qu.:53.69        3rd Qu.:27.81    3rd Qu.:2.952      3rd Qu.:30.48     
##  Max.   :0.027817   Max.   :67.58        Max.   :31.11    Max.   :4.196      Max.   :35.15     
##                                                                                                
##  CWM_LDMC_historic Fast_Slow_Gradient_historic  Ts_mean_30d       WHK_mean_30d      LUI_historic   
##  Min.   :0.2182    Min.   :-3.1286             Min.   :-2.0400   Min.   :-19.890   Min.   :0.5538  
##  1st Qu.:0.2727    1st Qu.:-1.1092             1st Qu.:-0.4650   1st Qu.: -1.597   1st Qu.:1.2253  
##  Median :0.2925    Median :-0.3014             Median : 0.1600   Median :  1.690   Median :1.5870  
##  Mean   :0.2916    Mean   : 0.0000             Mean   : 0.4952   Mean   :  2.185   Mean   :1.6222  
##  3rd Qu.:0.3101    3rd Qu.: 0.9908             3rd Qu.: 0.9650   3rd Qu.:  6.332   3rd Qu.:2.0109  
##  Max.   :0.3866    Max.   : 4.5679             Max.   : 9.8000   Max.   : 47.220   Max.   :3.9580  
##                                                NA's   :3         NA's   :2                           
##        rw                hw               Bodentyp   pH_historic   
##  Min.   :3515825   Min.   :5359200   Cambisol :52   Min.   :4.575  
##  1st Qu.:3536711   1st Qu.:5367490   Leptosol :33   1st Qu.:5.957  
##  Median :4389905   Median :5672850   Histosol :19   Median :6.655  
##  Mean   :4449212   Mean   :5639050   Stagnosol:18   Mean   :6.512  
##  3rd Qu.:5421250   3rd Qu.:5873388   Luvisol  : 9   3rd Qu.:7.150  
##  Max.   :5434900   Max.   :5891720   Gleysol  : 8   Max.   :7.450  
##                                      (Other)  :11                  
```

```
regression_data_all <- regression_data_all[-c(10, 24, 38, 43, 49, 50, 59, 81, 137), ]
# delete rows with missing values in the explanatory variables (10, 24, 59, 81 = missing values in climate
# data; 43, 50 = missing data in plant trait changes; 38, 49, 137 = missing data in plant biomass data) so
# that all models for one response variable are based on the same amount of samples (n)! Very important to
# be able to compare models at all.
ALB_reg <- regression_data_all[regression_data_all$Exploratory == "ALB", ]
```

First, we test the various spatial correlation structures in the basic model:

```
ALB_reg$ID <- 1

model <- lme(fungi ~ 1, data = ALB_reg, na.action = na.exclude, random = ~1 | ID, correlation = corExp(form = ~rw +
    hw, metric = "euclidean"), method = "ML")
model2 <- update(model, correlation = corGaus(form = ~rw + hw, metric = "euclidean"))
anova(model, model2)  #no improvement in AIC

##        Model df      AIC      BIC    logLik
## model      1  4 254.0798 261.2165 -123.0399
## model2     2  4 254.0798 261.2165 -123.0399

model4 <- update(model, correlation = corSpher(form = ~rw + hw, metric = "euclidean"))
anova(model, model4)  #no improvement in AIC

##        Model df      AIC      BIC    logLik
## model      1  4 254.0798 261.2165 -123.0399
## model4     2  4 254.0798 261.2165 -123.0399

model5 <- update(model, correlation = corLin(form = ~rw + hw, metric = "euclidean"))
anova(model, model5)  #no improvement in AIC

##        Model df      AIC      BIC    logLik
## model      1  4 254.0798 261.2165 -123.0399
## model5     2  4 254.0798 261.2165 -123.0399

model5 <- update(model, correlation = corRatio(form = ~rw + hw, metric = "euclidean"))
anova(model, model5)  #no improvement in AIC

##        Model df      AIC      BIC    logLik
## model      1  4 254.0798 261.2165 -123.0399
## model5     2  4 254.0798 261.2165 -123.0399

model <- lme(fungi ~ 1, data = ALB_reg, na.action = na.exclude, random = ~1 | ID, correlation = corExp(form = ~rw +
    hw, metric = "euclidean"), method = "ML")
```

No correlation structure is superior to exponential correlation structure in AIC values. Therefore this correlation structure is used in subsequent modelling.
We additionally test whether the use of a correlation structure is superior over the use of ”PlotID” (AEG01, AEG02, etc.) or soil type (Leptosol, Stagnosol, etc.) as random effects and whether a random effect is needed at all.

```
model6 <- lme(fungi ~ 1, data = ALB_reg, na.action = na.exclude, random = ~1 | PlotID, method = "ML")
anova(model, model6)  #improvement in AIC

##        Model df      AIC      BIC    logLik   Test      L.Ratio p-value
## model      1  4 254.0798 261.2165 -123.0399
## model6     2  3 252.0798 257.4323 -123.0399 1 vs 2 3.611785e-08  0.9998

model7 <- lme(fungi ~ 1, data = ALB_reg, na.action = na.exclude, random = ~1 | Bodentyp, method = "ML")
anova(model6, model7)  #no improvement in AIC

##        Model df      AIC      BIC    logLik
## model6     1  3 252.0798 257.4323 -123.0399
## model7     2  3 252.0798 257.4323 -123.0399

model8 <- lm(fungi ~ 1, data = ALB_reg, na.action = na.exclude)
AIC(model6, model8)  #improvement in AIC

##        df      AIC
## model6  3 252.0798
## model8  2 250.0798
```

The test shows that the use of a simple linear model without random effect gives the best result, i.e. the lowest AIC value. According to Occam's razor we therefore use the less complex linear model. Therefore the null model does not contain any random effects or correlation structures. The fit of the model residuals is tested with the following code:

```
model <- lm(fungi ~ 1, data = ALB_reg, na.action = na.exclude)

# plot(model, cex=0.7, cex.lab=0.8, cex.axis=0.7)

# model_residuals <- residuals(model) hist(model_residuals, cex=0.8, cex.lab=0.8, cex.axis=0.8, main='')
# legend('topleft', 'a)', bty='n', cex=1.5)

# qqnorm(model£residuals, cex=0.8, cex.lab=0.8, cex.axis=0.8, main='') legend('topleft', 'b)', bty='n',
# cex=1.5)
```

The model residuals are reasonably normal and homogeniously distributed, i.e. we do not need to transform fungal PLFA.

Summary of the null model:

```
model <- lm(fungi ~ 1, data = ALB_reg, na.action = na.exclude)
summary.lm(model)

##
## Call:
## lm(formula = fungi ~ 1, data = ALB_reg, na.action = na.exclude)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.1361 -2.3913 -0.2587  2.7022  9.3330
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   6.0427     0.6046   9.994 8.78e-13 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.011 on 43 degrees of freedom

summary.aov(model)

##             Df Sum Sq Mean Sq F value Pr(>F)
## Residuals   43  691.6   16.08
```

In the next steps we construct the full model with all significant fixed effects.

1.1.1 Level 1: Environmental factors

```
model0 <- lm(fungi ~ 1, data = ALB_reg, na.action = na.exclude)

model1_1 <- lm(fungi ~ Ts_mean_30d, data = ALB_reg, na.action = na.exclude)
AIC(model0, model1_1)  #no improvement in AIC

##          df      AIC
## model0    2 250.0798
## model1_1  3 251.3933

model1_2 <- lm(fungi ~ WHK_mean_30d, data = ALB_reg, na.action = na.exclude)
AIC(model0, model1_2)  #no improvement in AIC

##          df      AIC
## model0    2 250.0798
## model1_2  3 252.0166

model1_3 <- lm(fungi ~ pH_historic, data = ALB_reg, na.action = na.exclude)
AIC(model0, model1_3)  #no improvement in AIC

##          df      AIC
## model0    2 250.0798
## model1_3  3 250.1930
```

In case of fungal PLFA, including the environmental parameters into the model does not improve it.

1.1.2 Level 2: Land management

The final model of Level 1 is now extended with the fixed effects of Level 2.

```
model2_0 <- lm(fungi ~ 1, data = ALB_reg, na.action = na.exclude)

model2_1 <- lm(fungi ~ LUI_historic, data = ALB_reg, na.action = na.exclude)
AIC(model2_0, model2_1)  #no improvement in AIC

##          df      AIC
## model2_0  2 250.0798
## model2_1  3 251.8976

model2_2 <- lm(fungi ~ LUI_change, data = ALB_reg, na.action = na.exclude)
AIC(model2_0, model2_2)  # improvement in AIC, but by less than 2

##          df      AIC
## model2_0  2 250.0798
## model2_2  3 249.5323
```

In case of fungal PLFA, the land management variables are not included into the model.

1.1.3 Level 3: pH-change

The final model of Level 2 is now extended with the fixed effects of Level 3.

```
model3_0 <- lm(fungi ~ 1, data = ALB_reg, na.action = na.exclude)

model3_1 <- lm(fungi ~ pH_change, data = ALB_reg, na.action = na.exclude)
AIC(model3_0, model3_1)  #no improvement in AIC

##          df      AIC
## model3_0  2 250.0798
## model3_1  3 252.0796
```

Including ΔpH does not improve the model.

1.1.4 Level 4: Plant functional traits

The final model of Level 3 is now extended with the fixed effects of Level 4.

```
model4_0 <- lm(fungi ~ 1, data = ALB_reg, na.action = na.exclude)

# CWM mycorrhizal intensity
model4_1 <- lm(fungi ~ CWM_Myc_int_change, data = ALB_reg, na.action = na.exclude)
AIC(model4_0, model4_1)  #no improvement in AIC

##          df      AIC
## model4_0  2 250.0798
## model4_1  3 250.8916

model4_2 <- lm(fungi ~ CWM_Myc_int_historic, data = ALB_reg, na.action = na.exclude)
AIC(model4_0, model4_2)  #no improvement in AIC

##          df      AIC
## model4_0  2 250.0798
## model4_2  3 251.7976

# CWM SLA
model4_3 <- lm(fungi ~ CWM_SLA_change, data = ALB_reg, na.action = na.exclude)
AIC(model4_0, model4_3)  #no improvement in AIC

##          df      AIC
## model4_0  2 250.0798
## model4_3  3 250.6761

model4_4 <- lm(fungi ~ CWM_SLA_historic, data = ALB_reg, na.action = na.exclude)
AIC(model4_0, model4_4)  # improvement in AIC

##          df      AIC
## model4_0  2 250.0798
## model4_4  3 247.6170

anova(model4_0, model4_4)  # is significant

## Analysis of Variance Table
##
## Model 1: fungi ~ 1
## Model 2: fungi ~ CWM_SLA_historic
##   Res.Df    RSS Df Sum of Sq      F  Pr(>F)
## 1     43 691.62
## 2     42 624.91  1    66.708 4.4834 0.04019 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# CWM leaf P:
model4_5 <- lm(fungi ~ CWM_leafP_change, data = ALB_reg, na.action = na.exclude)
AIC(model4_0, model4_5)  #no improvement in AIC

##          df      AIC
## model4_0  2 250.0798
## model4_5  3 251.2146

model4_6 <- lm(fungi ~ CWM_leafP_historic, data = ALB_reg, na.action = na.exclude)
AIC(model4_0, model4_6)  # improvement in AIC, but by less than 2

##          df      AIC
## model4_0  2 250.0798
## model4_6  3 249.8026

# CWM leaf N:
model4_7 <- lm(fungi ~ CWM_leafN_change, data = ALB_reg, na.action = na.exclude)
AIC(model4_0, model4_7)  # improvement in AIC, but by less than 2

##          df      AIC
## model4_0  2 250.0798
## model4_7  3 248.2631

model4_8 <- lm(fungi ~ CWM_leafN_historic, data = ALB_reg, na.action = na.exclude)
AIC(model4_0, model4_8)  #no improvement in AIC

##          df      AIC
## model4_0  2 250.0798
## model4_8  3 251.1075
```

The final model at the end of Level 4 includes CWM_SLA_historic.

1.1.5 Level 5: Plant biomass properties

The final model of Level 4 is now extended with the fixed effects of Level 5.

```
model5_0 <- lm(fungi ~ CWM_SLA_historic, data = ALB_reg, na.action = na.exclude)

model5_1 <- lm(fungi ~ CWM_SLA_historic + Plant_Biomass, data = ALB_reg, na.action = na.exclude)
AIC(model5_0, model5_1)  # no improvement in AIC

##          df      AIC
## model5_0  3 247.6170
## model5_1  4 249.6154

model5_2 <- lm(fungi ~ CWM_SLA_historic + Cellulose, data = ALB_reg, na.action = na.exclude)
AIC(model5_0, model5_2)  # no improvement in AIC

##          df      AIC
## model5_0  3 247.6170
## model5_2  4 249.0202

model5_3 <- lm(fungi ~ CWM_SLA_historic + Hemicellulosen, data = ALB_reg, na.action = na.exclude)
AIC(model5_0, model5_3)  # no improvement in AIC

##          df     AIC
## model5_0  3 247.617
## model5_3  4 249.615

model5_4 <- lm(fungi ~ CWM_SLA_historic + Lignin, data = ALB_reg, na.action = na.exclude)
AIC(model5_0, model5_4)  #no improvement in AIC

##          df      AIC
## model5_0  3 247.6170
## model5_4  4 249.1356

model5_5 <- lm(fungi ~ CWM_SLA_historic + Pfl_N, data = ALB_reg, na.action = na.exclude)
AIC(model5_0, model5_5)  #no improvement in AIC

##          df     AIC
## model5_0  3 247.617
## model5_5  4 249.357

model5_6 <- lm(fungi ~ CWM_SLA_historic + Pfl_P, data = ALB_reg, na.action = na.exclude)
AIC(model5_0, model5_6)  #no improvement in AIC

##          df      AIC
## model5_0  3 247.6170
## model5_6  4 249.6077

model5_7 <- lm(fungi ~ CWM_SLA_historic + Lignin_N_ratio, data = ALB_reg, na.action = na.exclude)
AIC(model5_0, model5_7)  #no improvement in AIC

##          df      AIC
## model5_0  3 247.6170
## model5_7  4 249.1818
```

After Level 5, CWM_SLA_historic remains in the model.

1.1.6 Final model

Fungal PLFA is best described by the linear model:
`lm(fungi∼CWM_SLA_historic, data=ALB_reg, na.action=na.exclude)`.

```
model_final <- lm(fungi ~ CWM_SLA_historic, data = ALB_reg, na.action = na.exclude)


sum_lm_model_final <- summary.lm(model_final)
sum_lm_model_final

##
## Call:
## lm(formula = fungi ~ CWM_SLA_historic, data = ALB_reg, na.action = na.exclude)
```

```
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -8.9026 -2.0607 -0.3797  2.3532  9.4044
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)       16.1222     4.7957   3.362  0.00166 **
## CWM_SLA_historic  -0.3950     0.1866  -2.117  0.04019 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.857 on 42 degrees of freedom
## Multiple R-squared:  0.09645,Adjusted R-squared:  0.07494
## F-statistic: 4.483 on 1 and 42 DF,  p-value: 0.04019
```

```
fstat <- sum_lm_model_final$fstatistic
pval <- pf(fstat[1], fstat[2], fstat[3], lower.tail = FALSE)

aov_model <- summary.aov(model_final)
aov_model
```

```
##                  Df Sum Sq Mean Sq F value Pr(>F)
## CWM_SLA_historic  1   66.7   66.71   4.483 0.0402 *
## Residuals        42  624.9   14.88
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# calculate the percent variance explained by each fixed effect:
SSY <- sum(aov_model[[1]][, 2])
SSY
```

```
## [1] 691.6184
```

```
SSR_1_percent <- (aov_model[[1]][, 2][1])/SSY * 100
SSR_1_percent
```

```
## [1] 9.645201
```

Calculating pseudo-r^2 and delta-AIC for the final model. Explained unique variance of dependent variables by independent variables and random effects is assessed following the approach of Nakagawa and Schielzeth (2013) using the function "sem.model.fits" of the "piecewiseSEM" package (Lefcheck, 2016). Thereby the marginal (independent variables) and conditional (random effects) pseudo-r^2 are calculated for the full final model and models reduced by the variables of significant levels, one for each level. By substracting the reduced model from the full final model, the marginal r^2 of the respective level is calculated, i.e. the respective variance explained by the level. The same procedure is used to calculate the delta AIC of each level.

```
# create dataframes to store calculated values
pseudo_r_model_ALB <- data.frame(Variable = NA, Class = NA, Family = NA, Link = NA, n = NA, total_AIC = NA,
    total_Marginal = NA, total_Conditional = NA, d_AIC_L_1 = NA, Var_L_1 = NA, d_AIC_L_2 = NA, Var_L_2 = NA,
    d_AIC_L_3 = NA, Var_L_3 = NA, d_AIC_L_4 = NA, Var_L_4 = NA, d_AIC_L_5 = NA, Var_L_5 = NA, d_AIC_Int = NA,
    Var_Int = NA)  # _Int = Interaction

models_ALB <- data.frame(Variable = NA, coef_intercept = NA, coef_fixed_1 = NA, coef_fixed_2 = NA, coef_fixed_3 = NA,
    coef_fixed_4 = NA, coef_random = NA)

# calculate full final model
model_final <- lm(fungi ~ CWM_SLA_historic, data = ALB_reg, na.action = na.exclude)
# calculate model without fixed effects of level 4
model_final_2 <- lm(fungi ~ 1, data = ALB_reg, na.action = na.exclude)

# extract model coefficients
model_call <- model_final$call
model_call
```

```
## lm(formula = fungi ~ CWM_SLA_historic, data = ALB_reg, na.action = na.exclude)
```

```
model_coef_intercept <- as.numeric(model_final$coefficients[[1]][1])
model_coef_fix_1 <- as.numeric(model_final$coefficients[[2]][1])
model_coef_fix_2 <- "NA"
model_coef_fix_3 <- "NA"
model_coef_fix_4 <- "NA"
model_coef_ran_1 <- "NA"

# write coefficients into respective data frame
models_ALB[1, c("Variable")] <- "fungi"
```

```
models_ALB[1, c("coef_intercept")] <- model_coef_intercept
models_ALB[1, c("coef_fixed_1")] <- model_coef_fix_1
models_ALB[1, c("coef_fixed_2")] <- model_coef_fix_2
models_ALB[1, c("coef_fixed_3")] <- model_coef_fix_3
models_ALB[1, c("coef_fixed_4")] <- model_coef_fix_4
models_ALB[1, c("coef_random")] <- model_coef_ran_1
# models_ALB

# calculate AIC for each of the models, AIC_0 = full model, AIC_4 = model without 4th level
AIC_0 <- AIC(model_final)
AIC_1 <- "NA"
AIC_2 <- "NA"
AIC_3 <- "NA"
AIC_4 <- AIC(model_final_2)
AIC_5 <- "NA"
AIC_Int <- "NA"

# calculate delta AIC between full model and model with the respective missing level
D_AIC_Level_1 <- "NA"
D_AIC_Level_2 <- "NA"
D_AIC_Level_3 <- "NA"
D_AIC_Level_4 <- AIC_0 - AIC_4
D_AIC_Level_5 <- "NA"
D_AIC_Int <- "NA"

# calculate marginal and conditional r-square for each of the models
fits_0 <- sem.model.fits(model_final)
fits_1 <- "NA"
fits_2 <- "NA"
fits_3 <- "NA"
fits_4 <- sem.model.fits(model_final_2)
fits_5 <- "NA"
fits_Int <- "NA"

# calculate delta r-square for each level, i.e. the r-square that can be attributed to the respective
# level
D_fits_Level_1 <- "NA"
D_fits_Level_2 <- "NA"
D_fits_Level_3 <- "NA"
D_fits_Level_4 <- fits_0[1, 5] - fits_4[1, 5]
D_fits_Level_5 <- "NA"
D_fits_Int <- "NA"

# write data into respective data frame
pseudo_r_model_ALB[1, c("Variable")] <- "fungi"

pseudo_r_model_ALB[1, c("Class", "Family", "Link", "n", "total_Marginal")] <- fits_0[1, c(1:5)]
pseudo_r_model_ALB[1, c("total_Conditional")] <- "NA"
pseudo_r_model_ALB[1, c("total_AIC")] <- AIC_0
pseudo_r_model_ALB[1, c("d_AIC_L_1")] <- D_AIC_Level_1
pseudo_r_model_ALB[1, c("Var_L_1")] <- D_fits_Level_1
pseudo_r_model_ALB[1, c("d_AIC_L_2")] <- D_AIC_Level_2
pseudo_r_model_ALB[1, c("Var_L_2")] <- D_fits_Level_2
pseudo_r_model_ALB[1, c("d_AIC_L_3")] <- D_AIC_Level_3
pseudo_r_model_ALB[1, c("Var_L_3")] <- D_fits_Level_3
pseudo_r_model_ALB[1, c("d_AIC_L_4")] <- D_AIC_Level_4
pseudo_r_model_ALB[1, c("Var_L_4")] <- D_fits_Level_4
pseudo_r_model_ALB[1, c("d_AIC_L_5")] <- D_AIC_Level_5
pseudo_r_model_ALB[1, c("Var_L_5")] <- D_fits_Level_5
pseudo_r_model_ALB[1, c("d_AIC_Int")] <- D_AIC_Int
pseudo_r_model_ALB[1, c("Var_Int")] <- D_fits_Int
# pseudo_r_model_ALB
```

Check for normal distribution and homoscedasticity of variance of model residuals.

```
# plot(model_final, cex=0.7, cex.lab=0.8, cex.axis=0.7)

# model_residuals <- residuals(model_final) #stores residuals hist(model_residuals, cex=0.8, cex.lab=0.8,
# cex.axis=0.8, main='') # plots a histogram legend('topleft', 'a)', bty='n', cex=1.5)

# qqnorm(model_final£residuals, cex=0.8, cex.lab=0.8, cex.axis=0.8, main='') legend('topleft', 'b)',
# bty='n', cex=1.5)
```

The residuals of the full model are reasonably well distributed.

The net change in fungal PLFA is best explained by the linear model `lm(fungi∼CWM_SLA_historic, data=ALB_reg, na.action=na.exclude)`.

Model details: residual standard error = 3.857 on 42 degrees of freedom, multiple $r^2 = 0.1$, adjusted $r^2 = 0.07$, F-statistics: 4.48 on 1 and 42, overall model significance: $p = 0.04$; percent explained variation for `CWM_SLA_historic`: 9.65 %.

Table 2: Parameter estimates of the full model on fungal PLFAs.

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	16.1222	4.7957	3.36	0.0017
CWM_SLA_historic	-0.3950	0.1866	-2.12	0.0402

Table 3: ANOVA table of the full model on fungal PLFAs.

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
CWM_SLA_historic	1	66.71	66.71	4.48	0.0402
Residuals	42	624.91	14.88		

Table 4: Table of model coefficients.

	Variable	coef_intercept	coef_fixed_1	coef_fixed_2	coef_fixed_3	coef_fixed_4	coef_random
1	fungi	16.12	-0.40	NA	NA	NA	NA

Table 5: Table of pseudo r^2 values. d = delta, AIC = Akaike's information criterion, L = level in hierarchical regression, Var = explained variance, Int = Interaction

Variable	Class	Family	Link	n	total_AIC	total_Marginal	total_Conditional	d_AIC_L_1	Var_L_1	d_AIC_L_2	Var_L_2	d_AIC_L_3	Var_L_3	d_AIC_L_4	Var_L_4	d_AIC_L_5	Var_L_5	d_AIC_Int	Var_Int
fungi	1	1	1	1	247.617013	0.09645201	NA	NA	NA	NA	NA	NA	NA	-2.46274618	0.09645201	NA	NA	NA	NA

The change in fungal PLFA between 2011 and 2014 depends on the historic CWM SLA.

2 Structural equation modelling

The data evaluation using structural equation models (SEMs) builds upon the results of the regression analyses. Based on the regression results, plant functional traits, plant biomass properties and pH played the major role in influencing soil microbiology. We now test, whether there are indirect effects of land-use intensity on soil microbial properties via other environmental properties. As random effects were kept only in 9 out of 42 microbial variabels in total and never in more than half per exploratory, random effects are not included in SEMs. Figure 1 of the manuscript shows the proposed SEMs with respective variables.

```
regression_data_all <- read.table(file = "regression_data_all_2017-11_R.txt", header = T)
ALB_reg <- regression_data_all[regression_data_all$Exploratory == "ALB", ]
```

Scale response/endogenous variables to yield similar data ranges for SEMs between [0;1].

```
ranging=function(x){
  (x-min(x,na.rm=T))/(max(x,na.rm=T)-min(x,na.rm=T))
}
```

```
ALB_reg_scaled <- ALB_reg[, -59]  #exclude soil type from data file

x <- 5
for (i in 6:59) {
    ALB_reg_scaled[, x + 1] <- ranging(ALB_reg_scaled[, i])
    x <- x + 1
}
```

2.1 SEM for fungi

First, we check the bivariate correlations of the variables that will be modelled using the function `pairs` and spearman rank correlation coefficients. The first output block shows the correlation coefficients r, the second the respective p-values.

```
##                      fungi LUI_change LUI_historic CWM_Myc_int_change CWM_Myc_int_historic
## fungi                 1.00      -0.34        -0.18               0.09                -0.06
## LUI_change           -0.34       1.00        -0.13               0.28                 0.04
## LUI_historic         -0.18      -0.13         1.00              -0.13                 0.32
## CWM_Myc_int_change    0.09       0.28        -0.13               1.00                -0.35
## CWM_Myc_int_historic -0.06       0.04         0.32              -0.35                 1.00
## CWM_leafP_historic   -0.28       0.11         0.71              -0.12                 0.38
## CWM_leafP_change     -0.10      -0.02         0.21              -0.04                 0.01
## Plant_Biomass         0.04      -0.10         0.10              -0.02                -0.19
## Cellulose            -0.08      -0.12         0.27               0.01                -0.16
## Lignin               -0.12       0.11         0.07               0.01                -0.01
##                      CWM_leafP_historic CWM_leafP_change Plant_Biomass Cellulose Lignin
## fungi                             -0.28            -0.10          0.04     -0.08  -0.12
## LUI_change                         0.11            -0.02         -0.10     -0.12   0.11
## LUI_historic                       0.71             0.21          0.10      0.27   0.07
## CWM_Myc_int_change                -0.12            -0.04         -0.02      0.01   0.01
## CWM_Myc_int_historic               0.38             0.01         -0.19     -0.16  -0.01
## CWM_leafP_historic                 1.00             0.06          0.13      0.21   0.11
## CWM_leafP_change                   0.06             1.00          0.07      0.10   0.14
## Plant_Biomass                      0.13             0.07          1.00      0.58  -0.23
## Cellulose                          0.21             0.10          0.58      1.00  -0.09
## Lignin                             0.11             0.14         -0.23     -0.09   1.00
##
## n
##                      fungi LUI_change LUI_historic CWM_Myc_int_change CWM_Myc_int_historic
## fungi                   50         50           50                 48                   50
## LUI_change              50         50           50                 48                   50
## LUI_historic            50         50           50                 48                   50
## CWM_Myc_int_change      48         48           48                 48                   48
## CWM_Myc_int_historic    50         50           50                 48                   50
## CWM_leafP_historic      50         50           50                 48                   50
## CWM_leafP_change        48         48           48                 48                   48
## Plant_Biomass           50         50           50                 48                   50
## Cellulose               48         48           48                 46                   48
## Lignin                  48         48           48                 46                   48
```

```
##                      CWM_leafP_historic CWM_leafP_change Plant_Biomass Cellulose Lignin
## fungi                                50               48            50        48     48
## LUI_change                           50               48            50        48     48
## LUI_historic                         50               48            50        48     48
## CWM_Myc_int_change                   48               48            48        46     46
## CWM_Myc_int_historic                 50               48            50        48     48
## CWM_leafP_historic                   50               48            50        48     48
## CWM_leafP_change                     48               48            48        46     46
## Plant_Biomass                        50               48            50        48     48
## Cellulose                            48               46            48        48     48
## Lignin                               48               46            48        48     48
##
## P
##                      fungi  LUI_change LUI_historic CWM_Myc_int_change CWM_Myc_int_historic
## fungi                       0.0145     0.2099       0.5396             0.6927
## LUI_change           0.0145            0.3643       0.0557             0.7639
## LUI_historic         0.2099 0.3643                  0.3829             0.0250
## CWM_Myc_int_change   0.5396 0.0557     0.3829                          0.0146
## CWM_Myc_int_historic 0.6927 0.7639     0.0250       0.0146
## CWM_leafP_historic   0.0511 0.4588     0.0000       0.4138             0.0063
## CWM_leafP_change     0.5046 0.8876     0.1535       0.8073             0.9422
## Plant_Biomass        0.7852 0.4764     0.4793       0.8899             0.1822
## Cellulose            0.5687 0.4172     0.0616       0.9329             0.2914
## Lignin               0.4004 0.4722     0.6269       0.9497             0.9451
##                      CWM_leafP_historic CWM_leafP_change Plant_Biomass Cellulose Lignin
## fungi                0.0511             0.5046           0.7852        0.5687    0.4004
## LUI_change           0.4588             0.8876           0.4764        0.4172    0.4722
## LUI_historic         0.0000             0.1535           0.4793        0.0616    0.6269
## CWM_Myc_int_change   0.4138             0.8073           0.8899        0.9329    0.9497
## CWM_Myc_int_historic 0.0063             0.9422           0.1822        0.2914    0.9451
## CWM_leafP_historic                      0.6885           0.3751        0.1474    0.4427
## CWM_leafP_change     0.6885                              0.6243        0.4919    0.3409
## Plant_Biomass        0.3751             0.6243                         0.0000    0.1172
## Cellulose            0.1474             0.4919           0.0000                  0.5401
## Lignin               0.4427             0.3409           0.1172        0.5401
```

None of the variables are highly correlated and therefore provide unique pieces of information.
Create separate linear models fitted with `lm` contained in one list called ”mymodels”. So that we can call for all the models in one.

```
fungi_ALB_models=list(
model1=lm(LUI_change ~ LUI_historic, data=ALB_reg),
model2=lm(CWM_leafP_historic ~ LUI_historic, data=ALB_reg),
model3=lm(CWM_leafP_change ~ LUI_change, data=ALB_reg),
model4=lm(fungi ~ CWM_leafP_historic, data=ALB_reg),
model5=lm(fungi ~ CWM_leafP_change, data=ALB_reg),
model6=lm(fungi ~ LUI_historic, data=ALB_reg),
model7=lm(fungi ~ LUI_change, data=ALB_reg)
)
```

Show the coefficients of all models at ones using `lapply`.

```
lapply(fungi_ALB_models, coef)  #extract intercepts and slopes

## $model1
##  (Intercept) LUI_historic
##    0.1648718   -0.1027096
##
## $model2
##  (Intercept) LUI_historic
##    1.6025010    0.5503945
##
## $model3
## (Intercept)  LUI_change
## -0.01117264  0.04941849
##
## $model4
##        (Intercept) CWM_leafP_historic
##          10.703350          -1.914697
##
## $model5
##      (Intercept) CWM_leafP_change
##         5.902697        -2.293037
##
## $model6
##  (Intercept) LUI_historic
##    6.7081902   -0.4804373
##
```

```
## $model7
## (Intercept)  LUI_change
##    5.929117   -2.162285
```

2.1.1 First SEM

First SEM:
We only provide the output of the best fitted model here.

SEM with `lavaan`; first create a text object with the connection:

```
SEM_fungi_ALB <- "
#direct effects
CWM_leafP_historic ~ a*LUI_historic
CWM_leafP_change ~ b*LUI_change
fungi ~ c*CWM_leafP_historic
fungi ~ d*CWM_leafP_change
fungi ~ e*LUI_historic
fungi ~ f*LUI_change

#correlation LUIs
LUI_historic ~~ g*LUI_change

#indirect effects on MO-variable (compound paths)
LUI_hist_in := a * c
LUI_change_in :=  b * d

#total effects on MO-variable
LUI_hist_te := e + (a*c)
LUI_change_te :=  f + (b*d)

#total correlations on MO-variable
LUI_hist_tc := e + (a*c) + (g*f) + (g*b*d)
LUI_change_tc :=  f + (b*d) + (g*e) + (g*a*c)
"
## CWM_leafP_historic ~~ CWM_leafP_change ##taken out, as path is not significant and increases AIC model
## improvement with separated paths via CWM_leafP_historic and CWM_leafP_change -> model fit assessable

# SEM_fungi_ALB output:

# [1] '\n#direct effects\nCWM_leafP_historic ~ a*LUI_historic\nCWM_leafP_change ~ b*LUI_change\nfungi
# ~ c*CWM_leafP_historic\nfungi ~ d*CWM_leafP_change\nfungi ~ e*LUI_historic\nfungi ~
# f*LUI_change\n\n#correlation LUIs\nLUI_historic ~~ g*LUI_change\n\n#indirect effects on MO-variable
# (compound paths)\nLUI_hist_in := a * c\nLUI_change_in := b * d\n\n#total effects on
# MO-variable\nLUI_hist_te := e + (a*c)\nLUI_change_te := f + (b*d)\n\n#total correlations on
# MO-variable\nLUI_hist_tc := e + (a*c) + (g*f) + (g*b*d)\nLUI_change_tc := f + (b*d) + (g*e) +
# (g*a*c)\n'
```

SEM output:

```
sem.model1 <- sem(SEM_fungi_ALB, data = ALB_reg_scaled)
summary(sem.model1, fit.measures = T, rsq = T)

## lavaan 0.6-3 ended normally after 41 iterations
##
##   Optimization method                           NLMINB
##   Number of free parameters                         12
##
##                                                   Used       Total
##   Number of observations                            48          50
##
##   Estimator                                         ML
##   Model Fit Test Statistic                       6.308
##   Degrees of freedom                                 3
##   P-value (Chi-square)                           0.098
##
## Model test baseline model:
##
##   Minimum Function Test Statistic               49.824
##   Degrees of freedom                                10
##   P-value                                        0.000
##
## User model versus baseline model:
##
##   Comparative Fit Index (CFI)                    0.917
##   Tucker-Lewis Index (TLI)                       0.723
```

```
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)                 25.776
##   Loglikelihood unrestricted model (H1)         28.930
##
##   Number of free parameters                         12
##   Akaike (AIC)                                 -27.552
##   Bayesian (BIC)                                -5.098
##   Sample-size adjusted Bayesian (BIC)          -42.744
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                          0.152
##   90 Percent Confidence Interval          0.000  0.319
##   P-value RMSEA <= 0.05                          0.131
##
## Standardized Root Mean Square Residual:
##
##   SRMR                                           0.070
##
## Parameter Estimates:
##
##   Information                                 Expected
##   Information saturated (h1) model          Structured
##   Standard Errors                             Standard
##
## Regressions:
##                        Estimate  Std.Err  z-value  P(>|z|)
##   CWM_leafP_historic ~
##     LUI_histrc (a)        1.038    0.144    7.225    0.000
##   CWM_leafP_change ~
##     LUI_change (b)        0.034    0.060    0.568    0.570
##   fungi ~
##     CWM_lfP_hs (c)       -0.261    0.152   -1.716    0.086
##     CWM_lfP_ch (d)       -0.176    0.160   -1.101    0.271
##     LUI_histrc (e)        0.180    0.219    0.822    0.411
##     LUI_change (f)       -0.095    0.067   -1.412    0.158
##
## Covariances:
##                    Estimate  Std.Err  z-value  P(>|z|)
##   LUI_historic ~~
##     LUI_change (g)   -0.009    0.011   -0.795    0.426
##
## Variances:
##                    Estimate  Std.Err  z-value  P(>|z|)
##    .CWM_lefP_hstrc    0.034    0.007    4.899    0.000
##    .CWM_leafP_chng    0.031    0.006    4.899    0.000
##    .fungi             0.038    0.008    4.899    0.000
##     LUI_historic      0.034    0.007    4.899    0.000
##     LUI_change        0.177    0.036    4.899    0.000
##
## R-Square:
##                    Estimate
##     CWM_lefP_hstrc    0.521
##     CWM_leafP_chng    0.007
##     fungi             0.121
##
## Defined Parameters:
##                    Estimate  Std.Err  z-value  P(>|z|)
##     LUI_hist_in      -0.271    0.162   -1.670    0.095
##     LUI_change_in    -0.006    0.012   -0.505    0.614
##     LUI_hist_te      -0.090    0.157   -0.576    0.564
##     LUI_change_te    -0.101    0.068   -1.488    0.137
##     LUI_hist_tc      -0.090    0.157   -0.571    0.568
##     LUI_change_tc    -0.100    0.068   -1.479    0.139
```

Tables for summarized model results:

```
SEM_estimates_table_fungi <- data.frame(Exploratory = NA, resp_variable = NA, mediator = NA, lhs = NA, op = NA,
    rhs = NA, label = NA, est = NA, se = NA, z = NA, pvalue = NA, est.std = NA, se.std = NA, z.std = NA, pvalue.std = NA)

SEM_estimates_table_fungi[1:18, 1] <- "ALB"
SEM_estimates_table_fungi[1:18, 2] <- "fungi"
SEM_estimates_table_fungi[1:18, 3] <- "CWM_leaf_P"
SEM_estimates_table_fungi[1:18, 4:11] <- parameterEstimates(sem.model1)[, 1:8]
SEM_estimates_table_fungi[1:18, 12:15] <- standardizedSolution(sem.model1)[, 4:7]

SEM_estimates_table_fungi[, 8:15] <- round(SEM_estimates_table_fungi[, 8:15], 3)
```

```
SEM_model_fit_table_fungi <- data.frame(Exploratory = NA, resp_variable = NA, mediator = NA, ntotal = NA,
    npar = NA, chisq = NA, df = NA, pvalue = NA, rmsea = NA, rmsea.pvalue = NA, srmr = NA, baseline.chisq = NA,
    baseline.df = NA, aic = NA, O2E = NA)  #O2E = observations/estimated Parameters

SEM_model_fit_table_fungi[1, 1] <- "ALB"
SEM_model_fit_table_fungi[1, 2] <- "fungi"
SEM_model_fit_table_fungi[1, 3] <- "CWM_leaf_P"
SEM_model_fit_table_fungi[1, 4:14] <- fitMeasures(sem.model1, c("ntotal", "npar", "chisq", "df", "pvalue",
    "rmsea", "rmsea.pvalue", "srmr", "baseline.chisq", "baseline.df", "aic"))

SEM_model_fit_table_fungi[1, 15] <- SEM_model_fit_table_fungi$ntotal/SEM_model_fit_table_fungi$npar

SEM_rsquare_table_fungi <- data.frame(Exploratory = NA, resp_variable = NA, mediator = NA, rsq_m_hist = NA,
    rsq_m_chg = NA, rsq_MO = NA)  #rsq_m_hist, rsq_m_chg and rsq_MO need to be taken out of model output by hand
SEM_rsquare_table_fungi[1, 1] <- "ALB"
SEM_rsquare_table_fungi[1, 2] <- "fungi"
SEM_rsquare_table_fungi[1, 3] <- "CWM_leaf_P"
SEM_rsquare_table_fungi[1, 4] <- 0.521
SEM_rsquare_table_fungi[1, 5] <- 0.007
SEM_rsquare_table_fungi[1, 6] <- 0.121
```

2.1.2 Second SEM

Second model - the mediator is the plant functional trait variable that had the second strongest influence on the response variable in regression analysis.

```
# SEM_fungi_ALB=' #direct effects CWM_Myc_int_historic ~ a*LUI_historic CWM_Myc_int_change ~ b*LUI_change
# fungi ~ c*CWM_Myc_int_historic fungi ~ d*CWM_Myc_int_change fungi ~ e*LUI_historic fungi ~ f*LUI_change
# #correlation LUIs LUI_historic ~~ g*LUI_change #indirect effects on MO-variable (compound paths)
# LUI_hist_in := a * c LUI_change_in := b * d #total effects on MO-variable LUI_hist_te := e + (a*c)
# LUI_change_te := f + (b*d) #total correlations on MO-variable LUI_hist_tc := e + (a*c) + (g*f) + (g*b*d)
# LUI_change_tc := f + (b*d) + (g*e) + (g*a*c) ' CWM_Myc_int_historic ~~ CWM_Myc_int_change ##taken out,
# as path is not significant and increases AIC model improvement with separated paths via
# CWM_Myc_int_historic and CWM_Myc_int_change -> model fit assessable SEM_fungi_ALB
```

SEM output:

```
# sem.model<-sem(SEM_fungi_ALB, data = ALB_reg_scaled) summary(sem.model, fit.measures=T, rsq=T)
```

Extract values from model and summarize them in tables:

```
# SEM_estimates_table_fungi[19:36,1]<-'ALB' SEM_estimates_table_fungi[19:36,2]<-'fungi'
# SEM_estimates_table_fungi[19:36,3]<-'CWM_Myc_int'
# SEM_estimates_table_fungi[19:36,4:11]<-parameterEstimates(sem.model)[,1:8]
# SEM_estimates_table_fungi[19:36,12:15]<-standardizedSolution(sem.model)[,4:7]
# SEM_estimates_table_fungi[,8:15]<-round(SEM_estimates_table_fungi[,8:15],3)
# SEM_model_fit_table_fungi[2,1]<-'ALB' SEM_model_fit_table_fungi[2,2]<-'fungi'
# SEM_model_fit_table_fungi[2,3]<-'CWM_Myc_int' SEM_model_fit_table_fungi[2,4:14 ]<-fitMeasures(sem.model,
# c('ntotal', 'npar', 'chisq', 'df', 'pvalue', 'rmsea', 'rmsea.pvalue', 'srmr', 'baseline.chisq',
# 'baseline.df', 'aic')) SEM_model_fit_table_fungi[2,15 ]<-SEM_model_fit_table_fungi£ntotal[2] /
# SEM_model_fit_table_fungi£npar[2] SEM_rsquare_table_fungi[2,1]<-'ALB'
# SEM_rsquare_table_fungi[2,2]<-'fungi' SEM_rsquare_table_fungi[2,3]<-'CWM_Myc_int'
# SEM_rsquare_table_fungi[2,4]<-0.083 SEM_rsquare_table_fungi[2,5]<-0.090
# SEM_rsquare_table_fungi[2,6]<-0.143
```

2.1.3 Third SEM

Third model - the mediator is the plant biomass variable that had the strongest influence on the response variable in regression analysis. As plant biomass and plant biomass cellulose content are strongly correlated, Plant Biomass was chosen as it is the variable with the stronger input on various microbial variables in hierarchical regression modelling.

```
# SEM_fungi_ALB=' #direct effects Plant_Biomass ~ a*LUI_historic Plant_Biomass ~ b*LUI_change fungi ~
# c*Plant_Biomass #fungi ~ d*Plant_Biomass fungi ~ e*LUI_historic fungi ~ f*LUI_change #correlation LUIs
# LUI_historic ~~ g*LUI_change #indirect effects on MO-variable (compound paths) LUI_hist_in := a * c
# LUI_change_in := b * c #total effects on MO-variable LUI_hist_te := e + (a*c) LUI_change_te := f + (b*c)
# #total correlations on MO-variable LUI_hist_tc := e + (a*c) + (g*f) + (g*b*c) LUI_change_tc := f + (b*c)
# + (g*e) + (g*a*c) '

# SEM_fungi_ALB
```

SEM output:

```
# sem.model<-sem(SEM_fungi_ALB, data = ALB_reg_scaled) summary(sem.model, fit.measures=T, rsq=T)
```

Extract values from model and summarize them in tables:

```
# SEM_estimates_table_fungi[37:52,1]<-'ALB' SEM_estimates_table_fungi[37:52,2]<-'fungi'
# SEM_estimates_table_fungi[37:52,3]<-'Plant_Biomass'
# SEM_estimates_table_fungi[37:52,4:11]<-parameterEstimates(sem.model)[,1:8]
# SEM_estimates_table_fungi[37:52,12:15]<-standardizedSolution(sem.model)[,4:7]
# SEM_estimates_table_fungi[,8:15]<-round(SEM_estimates_table_fungi[,8:15],3)
# SEM_model_fit_table_fungi[3,1]<-'ALB' SEM_model_fit_table_fungi[3,2]<-'fungi'
# SEM_model_fit_table_fungi[3,3]<-'Plant_Biomass' SEM_model_fit_table_fungi[3,4:14
# ]<-fitMeasures(sem.model, c('ntotal', 'npar', 'chisq', 'df', 'pvalue', 'rmsea', 'rmsea.pvalue', 'srmr',
# 'baseline.chisq', 'baseline.df', 'aic')) SEM_model_fit_table_fungi[3,15
# ]<-SEM_model_fit_table_fungi£ntotal[3] / SEM_model_fit_table_fungi£npar[3]
# SEM_rsquare_table_fungi[3,1]<-'ALB' SEM_rsquare_table_fungi[3,2]<-'fungi'
# SEM_rsquare_table_fungi[3,3]<-'Plant_Biomass' SEM_rsquare_table_fungi[3,4]<-NA
# SEM_rsquare_table_fungi[3,5]<-0.031 SEM_rsquare_table_fungi[3,6]<-0.077
```

2.1.4 Fourth SEM

Fourth model - the mediator is the plant biomass variable that had the second strongest influence on the response variable in regression analysis after plant biomass and its cellulose content, i.e. plant biomass lignin content.

```
# SEM_fungi_ALB=' #direct effects Lignin ~ a*LUI_historic Lignin ~ b*LUI_change fungi ~ c*Lignin #fungi ~
# d*Lignin fungi ~ e*LUI_historic fungi ~ f*LUI_change #correlation LUIs LUI_historic ~~ g*LUI_change
# #indirect effects on MO-variable (compound paths) LUI_hist_in := a * c LUI_change_in := b * c #total
# effects on MO-variable LUI_hist_te := e + (a*c) LUI_change_te := f + (b*c) #total correlations on
# MO-variable LUI_hist_tc := e + (a*c) + (g*f) + (g*b*c) LUI_change_tc := f + (b*c) + (g*e) + (g*a*c) '

# SEM_fungi_ALB
```

SEM output:

```
# sem.model<-sem(SEM_fungi_ALB, data = ALB_reg_scaled) summary(sem.model, fit.measures=T, rsq=T)
```

Extract values from model and summarize them in tables:

```
# SEM_estimates_table_fungi[53:68,1]<-'ALB' SEM_estimates_table_fungi[53:68,2]<-'fungi'
# SEM_estimates_table_fungi[53:68,3]<-'Lignin'
# SEM_estimates_table_fungi[53:68,4:11]<-parameterEstimates(sem.model)[,1:8]
# SEM_estimates_table_fungi[53:68,12:15]<-standardizedSolution(sem.model)[,4:7]
# SEM_estimates_table_fungi[,8:15]<-round(SEM_estimates_table_fungi[,8:15],3)
# SEM_model_fit_table_fungi[4,1]<-'ALB' SEM_model_fit_table_fungi[4,2]<-'fungi'
# SEM_model_fit_table_fungi[4,3]<-'Lignin' SEM_model_fit_table_fungi[4,4:14 ]<-fitMeasures(sem.model,
# c('ntotal', 'npar', 'chisq', 'df', 'pvalue', 'rmsea', 'rmsea.pvalue', 'srmr', 'baseline.chisq',
# 'baseline.df', 'aic')) SEM_model_fit_table_fungi[4,15 ]<-SEM_model_fit_table_fungi£ntotal[4] /
# SEM_model_fit_table_fungi£npar[4] SEM_rsquare_table_fungi[4,1]<-'ALB'
# SEM_rsquare_table_fungi[4,2]<-'fungi' SEM_rsquare_table_fungi[4,3]<-'Lignin'
# SEM_rsquare_table_fungi[4,4]<-NA SEM_rsquare_table_fungi[4,5]<-0.006 SEM_rsquare_table_fungi[4,6]<-0.086
```

2.1.5 Fifth SEM

Fifth model - the mediator soil pH.

```
# SEM_fungi_ALB=' #direct effects pH_historic ~ a*LUI_historic pH_change ~ b*LUI_change fungi ~
# c*pH_historic fungi ~ d*pH_change fungi ~ e*LUI_historic fungi ~ f*LUI_change #correlation LUIs
# LUI_historic ~~ g*LUI_change #indirect effects on MO-variable (compound paths) LUI_hist_in := a * c
# LUI_change_in := b * d #total effects on MO-variable LUI_hist_te := e + (a*c) LUI_change_te := f + (b*d)
# #total correlations on MO-variable LUI_hist_tc := e + (a*c) + (g*f) + (g*b*d) LUI_change_tc := f + (b*d)
# + (g*e) + (g*a*c) ' pH_historic ~~ pH_change ##taken out, as path is not significant and increases AIC
# model improvement with separated paths via pH_historic and pH_change -> model fit assessable
# SEM_fungi_ALB
```

SEM output:

```
# sem.model<-sem(SEM_fungi_ALB, data = ALB_reg_scaled) summary(sem.model, fit.measures=T, rsq=T)
```

Extract values from model and summarize them in tables:

```
# SEM_estimates_table_fungi[69:86,1]<-'ALB' SEM_estimates_table_fungi[69:86,2]<-'fungi'
# SEM_estimates_table_fungi[69:86,3]<-'pH'
# SEM_estimates_table_fungi[69:86,4:11]<-parameterEstimates(sem.model)[,1:8]
# SEM_estimates_table_fungi[69:86,12:15]<-standardizedSolution(sem.model)[,4:7]
# SEM_estimates_table_fungi[,8:15]<-round(SEM_estimates_table_fungi[,8:15],3)
# SEM_model_fit_table_fungi[5,1]<-'ALB' SEM_model_fit_table_fungi[5,2]<-'fungi'
# SEM_model_fit_table_fungi[5,3]<-'pH' SEM_model_fit_table_fungi[5,4:14 ]<-fitMeasures(sem.model,
# c('ntotal', 'npar', 'chisq', 'df', 'pvalue', 'rmsea', 'rmsea.pvalue', 'srmr', 'baseline.chisq',
# 'baseline.df', 'aic')) SEM_model_fit_table_fungi[5,15 ]<-SEM_model_fit_table_fungi£ntotal[5] /
# SEM_model_fit_table_fungi£npar[5] SEM_rsquare_table_fungi[5,1]<-'ALB'
# SEM_rsquare_table_fungi[5,2]<-'fungi' SEM_rsquare_table_fungi[5,3]<-'pH'
# SEM_rsquare_table_fungi[5,4]<-0.009 SEM_rsquare_table_fungi[5,5]<-0.000
# SEM_rsquare_table_fungi[5,6]<-0.070 write.csv(SEM_estimates_table_fungi,
# 'SEM_estimates_table_fungi_ALB.csv') write.csv(SEM_model_fit_table_fungi,
# 'SEM_model_fit_table_fungi_ALB.csv') write.csv(SEM_rsquare_table_fungi,
# 'SEM_rsquare_table_fungi_ALB.csv')
```

2.1.6 SEM results

The following tables summarize the results of the SEM for fungal PLFAs of all five SEMs. According to the best model fit to the data, the model with the CWM of the plant functional trait leaf P was selected as final SEM for fungal PLFA in the Schwäbische Alb.

Table 6: SEM estimates for fungal PLFA of all models. Given are the unstandardized regression coefficients (est) with their standard error (se), z-value (z) and respective *p*-value (pvalue), as well as the standardized correlation coefficients (est.std) with their standard error (se.std), z-value (z.std) and *p*-value (pvalue.std) for each microbial variable (MO variable) and the five selected mediator variables. The single model paths are described by lhs = left hand side, op = operator, rhs = right hand side and if applicable the respective label of the path.

	Exploratory	resp_variable	mediator	lhs	op	rhs	label	est	se	z	pvalue	est.std	se.std	z.std	pvalue.std
1	ALB	fungi	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.22	0.00	0.72	0.07	10.44	0.00
2	ALB	fungi	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.03	0.06	0.57	0.57	0.08	0.14	0.57	0.57
3	ALB	fungi	CWM_leaf_P	fungi	~	CWM_leafP_historic	c	-0.26	0.15	-1.72	0.09	-0.34	0.19	-1.76	0.08
4	ALB	fungi	CWM_leaf_P	fungi	~	CWM_leafP_change	d	-0.18	0.16	-1.10	0.27	-0.15	0.13	-1.11	0.27
5	ALB	fungi	CWM_leaf_P	fungi	~	LUI_historic	e	0.18	0.22	0.82	0.41	0.16	0.20	0.83	0.41
6	ALB	fungi	CWM_leaf_P	fungi	~	LUI_change	f	-0.10	0.07	-1.41	0.16	-0.19	0.13	-1.44	0.15
7	ALB	fungi	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.43	-0.12	0.14	-0.81	0.42
8	ALB	fungi	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.00	0.48	0.10	4.80	0.00
9	ALB	fungi	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.00	0.99	0.02	42.42	0.00
10	ALB	fungi	CWM_leaf_P	fungi	~~	fungi		0.04	0.01	4.90	0.00	0.88	0.09	10.11	0.00
11	ALB	fungi	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.00	1.00	0.00		
12	ALB	fungi	CWM_leaf_P	LUI_change	~~	LUI_change		0.18	0.04	4.90	0.00	1.00	0.00		
13	ALB	fungi	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.27	0.16	-1.67	0.10	-0.24	0.14	-1.71	0.09
14	ALB	fungi	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.01	-0.50	0.61	-0.01	0.02	-0.51	0.61
15	ALB	fungi	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.09	0.16	-0.58	0.56	-0.08	0.14	-0.58	0.56
16	ALB	fungi	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.10	0.07	-1.49	0.14	-0.20	0.14	-1.52	0.13
17	ALB	fungi	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.09	0.16	-0.57	0.57	-0.06	0.14	-0.40	0.69
18	ALB	fungi	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.07	-1.48	0.14	-0.20	0.14	-1.45	0.15
19	ALB	fungi	CWM_Myc_int	CWM_Myc_int_historic	~	LUI_historic	a	0.38	0.18	2.08	0.04	0.29	0.13	2.18	0.03
20	ALB	fungi	CWM_Myc_int	CWM_Myc_int_change	~	LUI_change	b	0.13	0.06	2.18	0.03	0.30	0.13	2.29	0.02
21	ALB	fungi	CWM_Myc_int	fungi	~	CWM_Myc_int_historic	c	0.05	0.12	0.38	0.71	0.05	0.14	0.38	0.71
22	ALB	fungi	CWM_Myc_int	fungi	~	CWM_Myc_int_change	d	0.31	0.17	1.88	0.06	0.26	0.14	1.93	0.05
23	ALB	fungi	CWM_Myc_int	fungi	~	LUI_historic	e	-0.12	0.16	-0.78	0.43	-0.11	0.14	-0.79	0.43
24	ALB	fungi	CWM_Myc_int	fungi	~	LUI_change	f	-0.18	0.07	-2.50	0.01	-0.35	0.13	-2.63	0.01
25	ALB	fungi	CWM_Myc_int	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.43	-0.12	0.14	-0.81	0.42
26	ALB	fungi	CWM_Myc_int	CWM_Myc_int_historic	~~	CWM_Myc_int_historic		0.05	0.01	4.90	0.00	0.92	0.08	12.02	0.00
27	ALB	fungi	CWM_Myc_int	CWM_Myc_int_change	~~	CWM_Myc_int_change		0.03	0.01	4.90	0.00	0.91	0.08	11.52	0.00
28	ALB	fungi	CWM_Myc_int	fungi	~~	fungi		0.04	0.01	4.90	0.00	0.86	0.09	9.19	0.00
29	ALB	fungi	CWM_Myc_int	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.00	1.00	0.00		
30	ALB	fungi	CWM_Myc_int	LUI_change	~~	LUI_change		0.18	0.04	4.90	0.00	1.00	0.00		
31	ALB	fungi	CWM_Myc_int	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.05	0.37	0.71	0.01	0.04	0.37	0.71
32	ALB	fungi	CWM_Myc_int	LUI_change_in	:=	b*d	LUI_change_in	0.04	0.03	1.42	0.15	0.08	0.06	1.44	0.15
33	ALB	fungi	CWM_Myc_int	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.11	0.15	-0.70	0.48	-0.10	0.13	-0.71	0.48
34	ALB	fungi	CWM_Myc_int	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.14	0.07	-1.96	0.05	-0.27	0.13	-2.03	0.04
35	ALB	fungi	CWM_Myc_int	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.11	0.15	-0.70	0.49	-0.06	0.14	-0.46	0.65
36	ALB	fungi	CWM_Myc_int	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.14	0.07	-1.95	0.05	-0.26	0.13	-1.95	0.05
37	ALB	fungi	Plant_Biomass	Plant_Biomass	~	LUI_historic	a	0.19	0.16	1.17	0.24	0.16	0.14	1.18	0.24
38	ALB	fungi	Plant_Biomass	Plant_Biomass	~	LUI_change	b	-0.02	0.07	-0.29	0.77	-0.04	0.14	-0.29	0.77
39	ALB	fungi	Plant_Biomass	fungi	~	Plant_Biomass	c	-0.04	0.13	-0.31	0.76	-0.04	0.14	-0.31	0.76
40	ALB	fungi	Plant_Biomass	fungi	~	LUI_historic	e	-0.12	0.16	-0.80	0.42	-0.11	0.14	-0.80	0.42
41	ALB	fungi	Plant_Biomass	fungi	~	LUI_change	f	-0.13	0.06	-1.94	0.05	-0.27	0.13	-2.01	0.04
42	ALB	fungi	Plant_Biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.30	-0.15	0.14	-1.06	0.29
43	ALB	fungi	Plant_Biomass	Plant_Biomass	~~	Plant_Biomass	<U+0097>	0.04	0.01	5.00	0.00	0.97	0.05	20.22	0.00
44	ALB	fungi	Plant_Biomass	fungi	~~	fungi	<U+0097>	0.04	0.01	5.00	0.00	0.92	0.07	12.76	0.00
45	ALB	fungi	Plant_Biomass	LUI_historic	~~	LUI_historic	<U+0097>	0.03	0.01	5.00	0.00	1.00	0.00		
46	ALB	fungi	Plant_Biomass	LUI_change	~~	LUI_change	<U+0097>	0.19	0.04	5.00	0.00	1.00	0.00		
47	ALB	fungi	Plant_Biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.30	0.77	-0.01	0.02	-0.30	0.77
48	ALB	fungi	Plant_Biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.00	0.21	0.83	0.00	0.01	0.21	0.83
49	ALB	fungi	Plant_Biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.15	-0.86	0.39	-0.12	0.14	-0.86	0.39
50	ALB	fungi	Plant_Biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.12	0.06	-1.93	0.05	-0.26	0.13	-2.00	0.05
51	ALB	fungi	Plant_Biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.13	0.15	-0.85	0.40	-0.08	0.14	-0.56	0.57
52	ALB	fungi	Plant_Biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.12	0.06	-1.91	0.06	-0.25	0.13	-1.87	0.06
53	ALB	fungi	Lignin	Lignin	~	LUI_historic	a	0.02	0.19	0.13	0.90	0.02	0.14	0.13	0.90
54	ALB	fungi	Lignin	Lignin	~	LUI_change	b	0.04	0.08	0.54	0.59	0.08	0.14	0.54	0.59
55	ALB	fungi	Lignin	fungi	~	Lignin	c	-0.08	0.12	-0.71	0.48	-0.10	0.14	-0.71	0.47
56	ALB	fungi	Lignin	fungi	~	LUI_historic	e	-0.14	0.16	-0.87	0.39	-0.12	0.14	-0.87	0.38
57	ALB	fungi	Lignin	fungi	~	LUI_change	f	-0.12	0.07	-1.84	0.07	-0.26	0.14	-1.90	0.06
58	ALB	fungi	Lignin	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.34	-0.14	0.14	-0.98	0.33
59	ALB	fungi	Lignin	Lignin	~~	Lignin		0.06	0.01	4.90	0.00	0.99	0.02	44.28	0.00
60	ALB	fungi	Lignin	fungi	~~	fungi		0.04	0.01	4.90	0.00	0.91	0.08	11.82	0.00
61	ALB	fungi	Lignin	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.00	1.00	0.00		
62	ALB	fungi	Lignin	LUI_change	~~	LUI_change		0.20	0.04	4.90	0.00	1.00	0.00		
63	ALB	fungi	Lignin	LUI_hist_in	:=	a*c	LUI_hist_in	-0.00	0.02	-0.13	0.90	-0.00	0.01	-0.13	0.90
64	ALB	fungi	Lignin	LUI_change_in	:=	b*c	LUI_change_in	-0.00	0.01	-0.43	0.67	-0.01	0.02	-0.43	0.67
65	ALB	fungi	Lignin	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.14	0.16	-0.88	0.38	-0.12	0.14	-0.88	0.38
66	ALB	fungi	Lignin	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.12	0.07	-1.89	0.06	-0.26	0.14	-1.96	0.05

Continued on next page

Table 6: SEM estimates for fungal PLFA of all models. Given are the unstandardized regression coefficients (est) with their standard error (se), z-value (z) and respective *p*-value (pvalue), as well as the standardized correlation coefficients (est.std) with their standard error (se.std), z-value (z.std) and *p*-value (pvalue.std) for each microbial variable (MO variable) and the five selected mediator variables. The single model paths are described by lhs = left hand side, op = operator, rhs = right hand side and if applicable the respective label of the path.

	Exploratory	resp_variable	mediator	lhs	op	rhs	label	est	se	z	pvalue	est.std	se.std	z.std	pvalue.std
67	ALB	fungi	Lignin	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.14	0.16	-0.87	0.38	-0.09	0.14	-0.60	0.55
68	ALB	fungi	Lignin	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.12	0.07	-1.87	0.06	-0.25	0.14	-1.83	0.07
69	ALB	fungi	pH	pH_historic	~	LUI_historic	a	-0.12	0.19	-0.67	0.50	-0.09	0.14	-0.67	0.50
70	ALB	fungi	pH	pH_change	~	LUI_change	b	-0.00	0.06	-0.08	0.93	-0.01	0.14	-0.08	0.93
71	ALB	fungi	pH	fungi	~	pH_historic	c	0.11	0.11	0.94	0.35	0.13	0.14	0.95	0.34
72	ALB	fungi	pH	fungi	~	pH_change	d	0.00	0.14	0.01	0.99	0.00	0.14	0.01	0.99
73	ALB	fungi	pH	fungi	~	LUI_historic	e	-0.11	0.15	-0.72	0.47	-0.10	0.14	-0.72	0.47
74	ALB	fungi	pH	fungi	~	LUI_change	f	-0.10	0.06	-1.59	0.11	-0.22	0.14	-1.63	0.10
75	ALB	fungi	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.30	-0.15	0.14	-1.06	0.29
76	ALB	fungi	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.00	0.99	0.03	37.71	0.00
77	ALB	fungi	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.00	1.00	0.00	298.93	0.00
78	ALB	fungi	pH	fungi	~~	fungi		0.04	0.01	5.00	0.00	0.93	0.07	13.43	0.00
79	ALB	fungi	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.00	1.00	0.00		
80	ALB	fungi	pH	LUI_change	~~	LUI_change		0.19	0.04	5.00	0.00	1.00	0.00		
81	ALB	fungi	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.02	-0.54	0.59	-0.01	0.02	-0.54	0.59
82	ALB	fungi	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.00	-0.01	0.99	0.00	0.00	-0.01	0.99
83	ALB	fungi	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.12	0.15	-0.80	0.42	-0.11	0.14	-0.81	0.42
84	ALB	fungi	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.10	0.06	-1.59	0.11	-0.22	0.14	-1.63	0.10
85	ALB	fungi	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.12	0.15	-0.80	0.42	-0.08	0.14	-0.57	0.57
86	ALB	fungi	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.06	-1.58	0.12	-0.20	0.13	-1.51	0.13

Table 7: SEM model fit for fungal PLFA of all models. Given are the model fit values for the five tested mediator types. If the model with the lowest AIC value had a significant *p*-value of X^2, the model with the next lower AIC without a significant *p*-value of X^2 was chosen (according to the t-rule model fit based on chi-square tests could not be assessed for SEMs with plant biomass and lignin). ntotal = no. of samples, npar = no. of estimated parameters, df = degrees of freedom, p = *p*-value of X^2, rmsea = root means square error, rmsea.p = *p*-value of rmsea, AIC = Akaike's information criterion, O2E = ratio of observed samples:estimated parameters.

	Exploratory	resp_variable	mediator	ntotal	npar	chisq	df	pvalue	rmsea	rmsea.pvalue	srmr	baseline.chisq	baseline.df	aic	O2E
1	ALB	fungi	CWM_leaf_P	48	12	6.31	3	0.10	0.15	0.13	0.07	49.82	10	-27.55	4.00
2	ALB	fungi	CWM_Myc_int	48	12	9.23	3	0.03	0.21	0.04	0.10	25.54	10	-8.92	4.00
3	ALB	fungi	Plant_Biomass	50	10	0.00	0		0.00		0.00	6.64	6	13.77	5.00
4	ALB	fungi	Lignin	48	10	0.00	0		0.00		0.00	5.53	6	32.29	4.80
5	ALB	fungi	pH	50	12	8.72	3	0.03	0.20	0.05	0.10	14.92	10	9.91	4.17

Table 8: SEM r^2 values for fungal PLFA of all models. resp_variable = response variable, rsq_m_hist = r^2 of historic mediator variable, rsq_m_chg = r^2 of Δmediator variable, rsq_MO = r^2 of microbial, i.e. response variable.

	Exploratory	resp_variable	mediator	rsq_m_hist	rsq_m_chg	rsq_MO
1	ALB	fungi	CWM_leaf_P	0.52	0.01	0.12
2	ALB	fungi	CWM_Myc_int	0.08	0.09	0.14
3	ALB	fungi	Plant_Biomass		0.03	0.08
4	ALB	fungi	Lignin		0.01	0.09
5	ALB	fungi	pH	0.01	0.00	0.07

Supplementary Figures

Plant functional trait shifts explain concurrent changes in the structure and function of grassland soil microbial communities

Boeddinghaus, R. S., Marhan, S., Berner, D., Boch, S., Fischer, M., Hölzel, N., Kattge, J., Klaus, V. H., Kleinebecker, T., Oelmann, Y., Prati, D., Schäfer, D., Schöning, I., Schrumpf, M., Sorkau, E., Kandeler, E. & Manning, P.

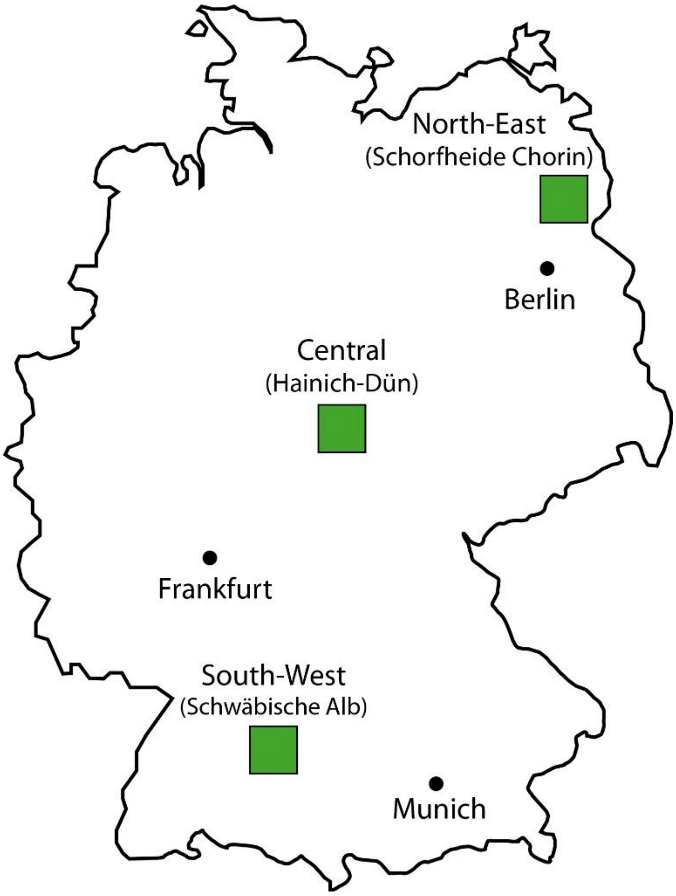


Figure S1: Location of the three investigated regions in Germany.

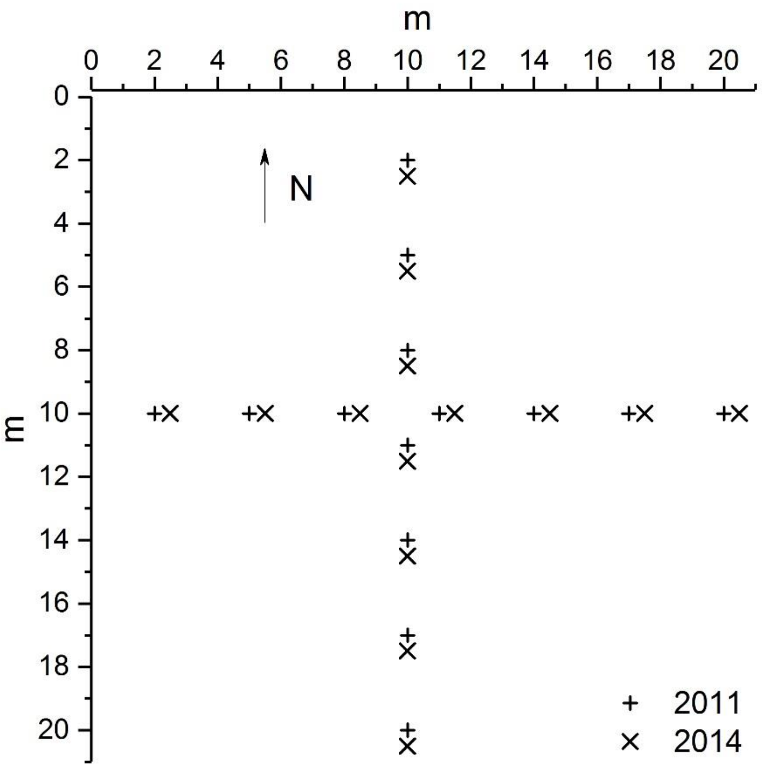
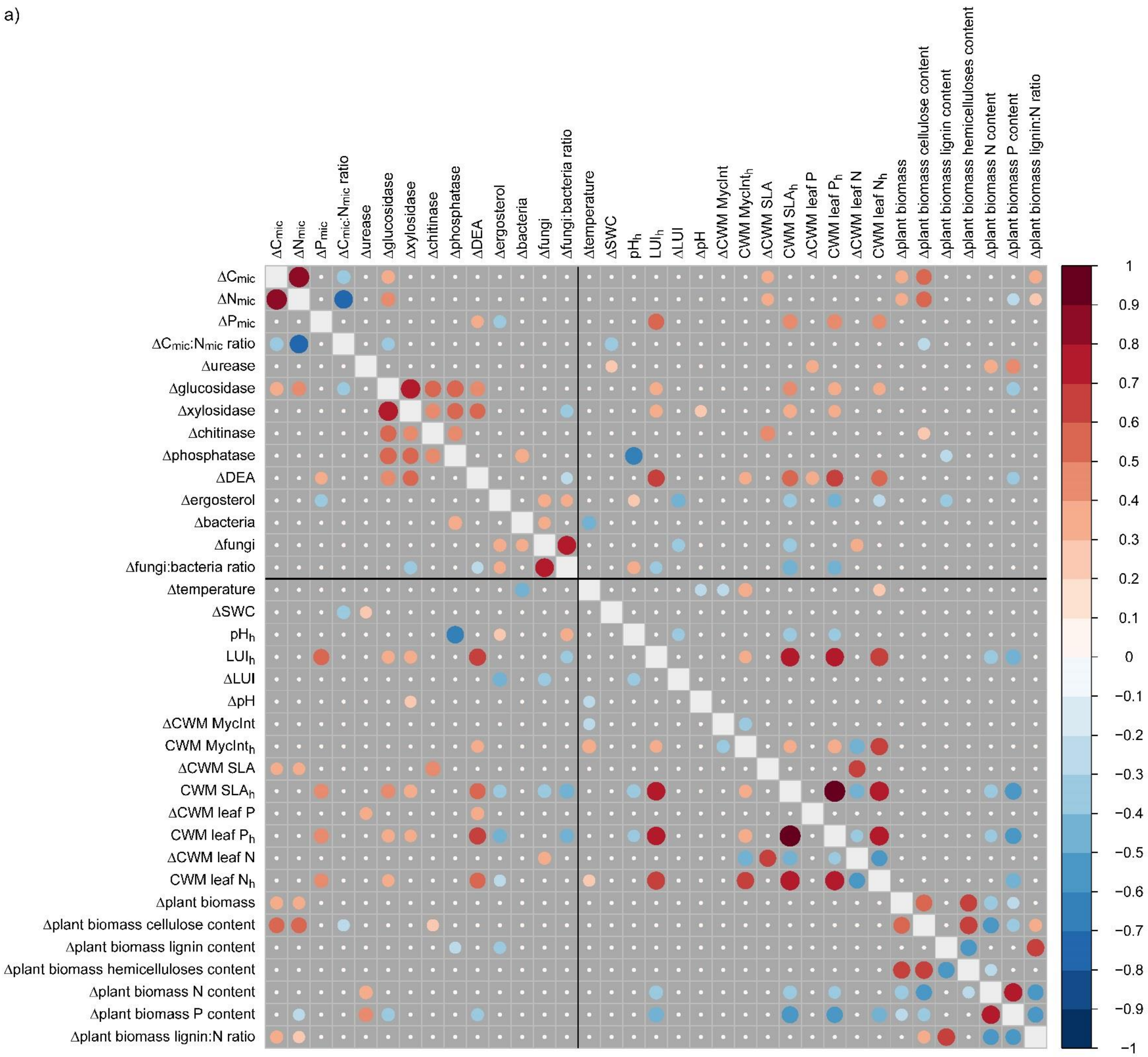
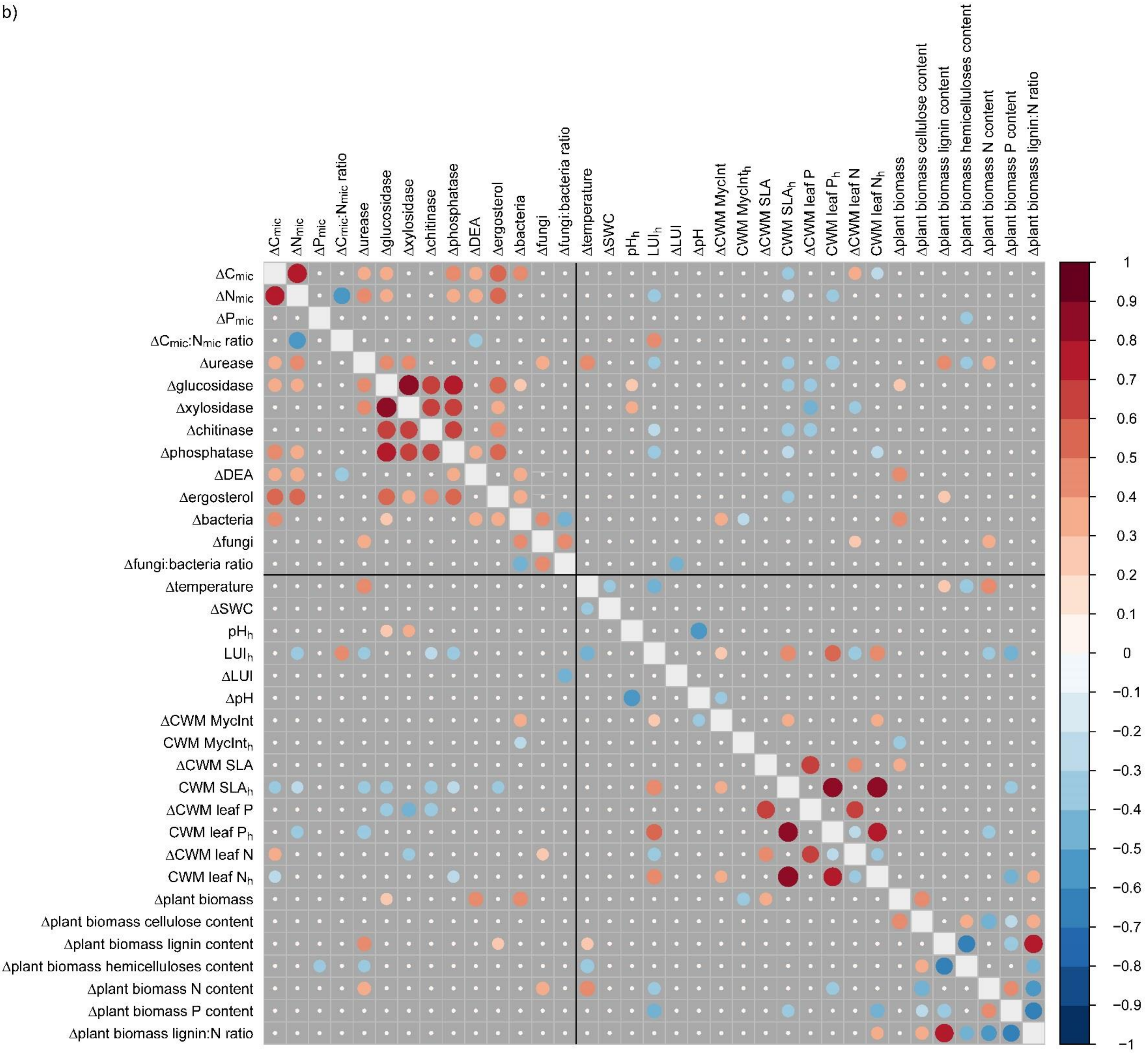


Figure S2: Sampling scheme for all grassland plots with sampling points of 2011 and 2014. In case obstacles such as shrubs or rocks inferred sampling at a selected spot, the sampling point was shifted along the transects by 1 m and the action protocolled.


a)
ΔC_{mic}
ΔN_{mic}
ΔP_{mic}
ΔC_{mic}:N_{mic} ratio
Δurease
Δglucosidase
Δxylosidase
Δchitinase
Δphosphatase
ΔDEA
Δergosterol
Δbacteria
Δfungi
Δfungi:bacteria ratio
Δtemperature
ΔSWC
pH_h
LUI_h
ΔLUI
ΔpH
ΔCWM MycInt
CWM $MycInt_h$
ΔCWM SLA
CWM SLA_h
ΔCWM leaf P
CWM leaf P_h
ΔCWM leaf N
CWM leaf N_h
Δplant biomass
Δplant biomass cellulose content
Δplant biomass lignin content
Δplant biomass hemicelluloses content
Δplant biomass N content
Δplant biomass P content
Δplant biomass lignin:N ratio
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
−0.1
−0.2
−0.3
−0.4
−0.5
−0.6
−0.7
−0.8
−0.9
−1

b)



ΔCmic
ΔNmic
ΔPmic
ΔCmic:Nmic ratio
Δurease
Δglucosidase
Δxylosidase
Δchitinase
Δphosphatase
ΔDEA
Δergosterol
Δbacteria
Δfungi
Δfungi:bacteria ratio
Δtemperature
ΔSWC
pHh
LUIh
ΔLUI
ΔpH
ΔCWM MycInt
CWM MycInth
ΔCWM SLA
CWM SLAh
ΔCWM leaf P
CWM leaf Ph
ΔCWM leaf N
CWM leaf Nh
Δplant biomass
Δplant biomass cellulose content
Δplant biomass lignin content
Δplant biomass hemicelluloses content
Δplant biomass N content
Δplant biomass P content
Δplant biomass lignin:N ratio
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
−0.1
−0.2
−0.3
−0.4
−0.5
−0.6
−0.7
−0.8
−0.9
−1

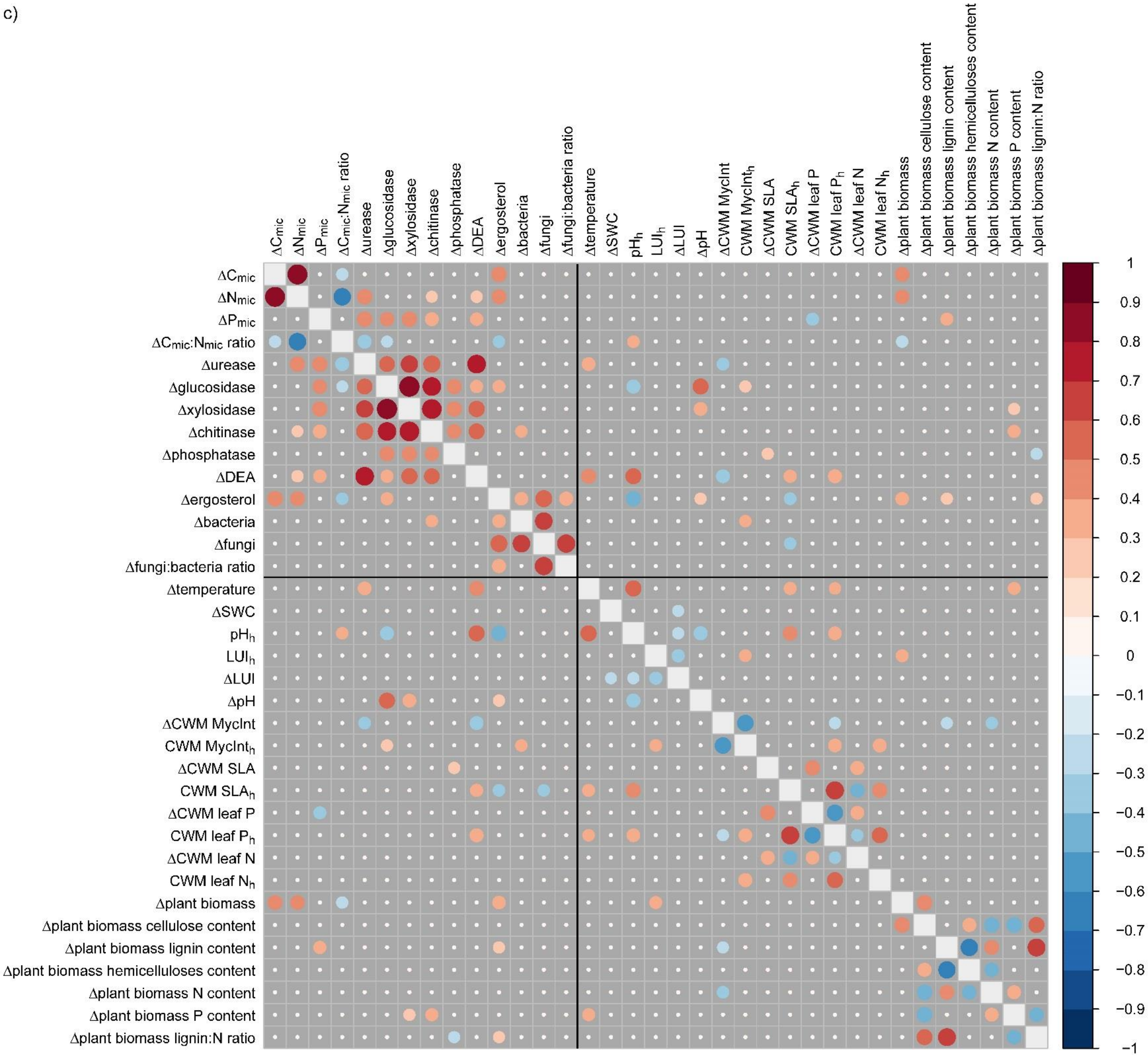


Figure S3: Spearman rank correlation coefficients (r) between fixed effects and response variables of linear models for the a) South-West, b) Central and c) North-East region. Only significant correlations are displayed.

Supplementary Tables

Plant functional trait shifts explain concurrent changes in the structure and function of grassland soil microbial communities

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Table S1: Hypothesized pathways in SEMs shown in Figures 1a and 1b. Land-use intensity influences soil microorganisms directly, but can also act indirectly as it affects properties of the microbial environment. Historic and change mediators were chosen as they were the most the most significant of the plausible mediator variables in hierarchical regression modelling. Effects can occur due to short term changes in the variables, but also via long-term legacy effects on changes in soil microorganisms (Δ). The nutrient content of a soil, for example, reflects past land-use intensity and influences the effect of new nutrient inputs by determining the level of nutrient limitation of soil biota and plants (Perring et al., 2016; Richter et al., 2000). In the case of grassland soil function for example, plant communities, and their functional properties, may take several years to fully respond to changes in land-use intensity (Poptcheva et al., 2009).

Path			**Hypotheses**	**References**
LUI_h	←→	ΔLUI	Historic land-use can influence future change in land use (e.g. highly intensive sites may be more likely to see LUI declines)	Perring et al. (2016)
LUI	→	Plant biomass	Nutrient availability to plants is increased by fertilisation, leading to higher plant biomass production	Milton (1940); Klaus et al. (2011)
LUI	→	Plant biomass lignin content	Fertilised and frequently disturbed (via mowing and grazing) environments select for fast growing plants with less structural components incorporating lignin	Reich (2014)
LUI	→	CWM of plant functional leaf traits (leaf P)	Fertilisation shifts plant communities towards fast growing species with high leaf P content	Pfestorf et al. (2013); Busch et al. (2018)
LUI	→	CWM MycInt	Fertilisation leads to reduction in root mycorrhization	Gehring and Whitham (1994); Titus and Lepš (2000); Treseder (2004)
LUI	→	pH	N fertilization leads to acidification of soils	Bardgett and McAlister (1999)
LUI	→	Δmicrobial properties	Nutrient availability to microbes is increased by fertilisation, with effects on microbial communities including increases in the abundance of bacteria relative to fungi.	de Vries et al. (2012)
			Changes in nutrient status affect microbial physiology and metabolism altering microbial biomass and soil enzyme activities	Kandeler and Eder (1993); Bardgett and Leemans (1995); Donnison et al. (2000)
Plant biomass	→	Δmicrobial properties	Increase in plant biomass leads to increase in litter inputs and rhizodeposition, which are important resources for soil microorganisms	Swinnen et al. (1995); Eisenhauer et al. (2017); Bardgett et al. (1998); Spohn et al. (2013)
Plant biomass lignin content	→	Δmicrobial properties	Plant litter with a high lignin input decomposes more slowly. Lignin rich inputs favour fungi over bacteria due to physiological differences.	Potthast et al. (2010); Sagova-Mareckova et al. (2011)
CWM of plant functional leaf traits (leaf P)	→	Δmicrobial properties	High quality litter inputs from plant communities possessing ‘fast’ traits favor bacteria over fungi	de Vries et al. (2012)
CWM MycInt	→	Δmicrobial properties	lower mycorrhization leads to lower total microbial biomass and less competition for nutrients between bacteria, saprotrophic fungi and mycorrhizal fungi	Tiunov and Scheu (2005)
pH	→	Δmicrobial properties	soil pH affects a wide range of microbial physiological process, including enzyme activities, and performance, affecting microbial community structure.	Fierer and Jackson (2006); Rousk et al. (2009); Fornara et al. (2011); Acosta-Martínez and Tabatabai (2011)

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Table S2: Characteristics of the three investigated regions with mean annual temperature (MAT), mean annual precipitation (MAP), elevation (m above sea level), areal spread of investigated sites, and soil types (and their number of occurrence) (Fischer et al. 2010), the latter determined after the World Reference Base of Soil Resources (IUSS Working Group WRB 2015), as well as soil texture (Solly et al. 2014).

region	MAT [°C]	MAP [mm]	elevation [m a.s.l.]	area [km²]	soil type (occurrence)	soil texture
South-West	6.0–7.0	700–1000	460–860	~422	Leptosol (33), Cambisol (17)	54 % clay, 41 % silt, 6 % sand
Central	6.5–8	500–800	285–550	~1300	Cambisol (28), Stagnosol (18),Vertisol (4)	42 % clay, 52 % silt, 6 % sand
North-East	8.0–8.5	500–600	3–140	~1300	Histosol (19), Luvisol (9), Gleysol (8), Albeluvisol (7), Cambisol (7)	17 % clay, 37 % silt, 45 % sand

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Table S3: Data used for the categories ‘historic’ and ‘change’. ‘Historic’ data was calculated as means of several years and includes the background value of pH (only one year of data available), while ‘change’ describes the net difference between two years.

Category	Variable	Time frame
historic	pH (background value)	2011
	LUI	2006 – 2010
	CWM MycInt	2008 – 2011
	CWM SLA	2008 – 2011
	CWM leaf P	2008 – 2011
	CWM leaf N	2008 – 2011
change	Temperature	2011, 2014
	Soil water content	2011, 2014
	pH	2011, 2014
	LUI	2010, 2013
	CWM MycInt	2011, 2014
	CWM SLA	2011, 2014
	CWM leaf P	2011, 2014
	CWM leaf N	2011, 2014
	Plant biomass	2011, 2014
	Plant biomass cellulose content	2011, 2014
	Plant biomass hemicelluloses content	2011, 2014
	Plant biomass lignin content	2011, 2014
	Plant biomass N content	2011, 2014
	Plant biomass P content	2011, 2014
	Plant biomass lignin:N ratio	2011, 2014

Table S4: Overview of data from Schwäbische Alb (South-West), Hainich-Dün (Central) and Schorfheide-Chorin (North-East). Given are minimum (min), maximum (max), median, mean, standard deviation (SD) and number of samples (N).

				South-West					
		Variable	**Unit**	**min**	**max**	**median**	**mean**	**SD**	**N**
response variable (change between 2011 and 2014)	microbial biomass	Cmic	µg C g^{-1} soil DM	-266.28	211.40	-0.06	3.71	99.52	50
		Nmic	µg N g^{-1} soil DM	-64.83	51.81	7.22	6.97	22.51	50
		Cmic:Nmic ratio		-2.09	0.85	-0.32	-0.38	0.69	50
		Pmic	µg P g^{-1} soil DM	-33.33	66.59	2.89	8.25	22.71	39
	enzyme activiy	beta-glucosidase	nmol MUF g^{-1} h^{-1}	-224.99	1183.15	486.15	503.17	328.26	50
		beta-xylosidase	nmol MUF g^{-1} h^{-1}	1.13	332.38	146.54	154.21	70.80	50
		chitinase	nmol MUF g^{-1} h^{-1}	-280.31	438.38	249.72	232.42	136.60	47
		urease	µg N g^{-1} DM 2h^{-1}	-21.12	208.64	59.45	62.52	45.24	50
		DEA	µg N$_2$O-N + N$_2$-N g^{-1} soil DM h^{-1}	0.07	7.74	1.72	1.96	1.52	50
		phosphatase	nmol MUF g^{-1} h^{-1}	-171.94	2025.45	841.54	888.13	455.30	50
	microbial community	bacteria	nmol FAME g^{-1} soil DM	-39.79	95.55	10.19	8.74	27.41	50
		gram negative bacteria	nmol FAME g^{-1} soil DM	-4.54	20.16	3.82	4.09	4.21	50
		gram positive bacteria	nmol FAME g^{-1} soil DM	-36.22	69.04	0.04	1.43	20.39	50
		fungi	nmol FAME g^{-1} soil DM	-3.09	15.38	5.78	5.93	3.82	50
		fungi:bacteria ratio		-0.02	0.15	0.04	0.05	0.04	50
		ergosterol	µg g^{-1} soil DM	-2.45	9.93	3.17	3.22	3.00	50
		invertebrates	nmol FAME g^{-1} soil DM	-0.71	3.06	1.31	1.24	0.75	50
		sum microbial PLFA	nmol FAME g^{-1} soil DM	17.66	291.08	102.01	112.54	53.65	50
explanatory variables	abiotic factors	temperature change	°C	-2.04	1.04	-0.52	-0.49	0.66	49
		soil water content change	% vol. of water holding capacity	-19.89	8.46	-1.48	-2.99	5.82	49
		pH change	in CaCl$_2$	-0.35	0.24	-0.08	-0.09	0.11	50
		pH historic	in CaCl$_2$	5.08	7.30	6.15	6.26	0.55	50
	land-use intensity	LUI change	dimensionless	-1.12	0.74	0.01	0.00	0.44	50
		LUI historic	dimensionless	0.55	3.96	1.66	1.62	0.63	50
		mowing change	no. of cuts per year	-0.89	1.61	-0.03	0.00	0.44	50
		fertilization change	kg N ha^{-1} a^{-1}	-3.33	4.04	0.00	0.00	1.35	50
		grazing change	livestock units d ha^{-1} year^{-1}	-3.90	1.37	0.00	0.00	1.01	50
	plant functional traits	CWM MycInt change	% colonized root length	-22.92	13.95	-1.36	-1.46	6.61	48
		CWM MycInt historic	% colonized root length	36.36	57.35	49.85	49.16	5.01	50
		CWM SLA change	mm² g^{-1} DM	-4.43	2.42	-0.13	-0.36	1.69	48
		CWM SLA historic	mm² g^{-1} DM	19.91	30.29	26.53	25.55	3.08	50
		CWM leaf P change	mg P g^{-1} DM	-0.97	0.48	0.02	-0.01	0.26	48
		CWM leaf P historic	mg P g^{-1} DM	1.55	3.33	2.58	2.49	0.48	50
		CWM leaf N change	mg N g^{-1} DM	-7.03	3.70	-0.60	-0.60	2.32	48
		CWM leaf N historic	mg N g^{-1} DM	19.03	32.75	28.52	27.34	3.62	50

Table S4 continued

		Variable	Unit	South-West					
				min	max	median	mean	SD	N
explanatory variables	plant biomass properties	plant biomass change	g m^{-2}	-74.45	602.95	124.23	164.37	145.01	50
		plant biomass cellulose content change	%	-2.60	8.65	1.53	2.08	2.93	48
		plant biomass hemicelluloses content change	%	-16.59	15.16	1.98	2.51	6.37	48
		plant biomass lignin content change	%	-1.27	2.75	0.43	0.51	0.99	48
		plant biomass lignin:N ratio change		-0.46	2.37	0.59	0.66	0.65	48
		plant biomass N content change	%	-1.06	0.31	-0.27	-0.29	0.34	48
		plant biomass P content change	%	-0.08	0.14	0.05	0.04	0.05	48
	excluded	fast-slow gradient change	site scores PC1	-3.38	2.37	-0.17	-0.19	1.10	48
		fast-slow gradient historic	site scores PC1	-2.61	4.57	-0.08	0.57	1.89	50
		Rao's Q change	index	-0.01	0.01	0.00	0.00	0.00	48
		Rao's Q historic	index	0.01	0.02	0.02	0.02	0.00	50
		number of species change	count	-6.00	21.00	4.00	4.42	4.43	48
		number of species historic	count	15.75	52.25	27.88	30.58	8.93	50
		number of grasses change	count	-6.00	8.00	0.00	0.20	2.62	49
		number of herbs change	count	-15.00	10.00	1.00	1.02	3.73	49
		number of legumes change	count	-3.00	2.00	0.00	-0.35	1.20	49
background variables (change between 2011 and 2014)		bulk density	g cm^{-3}	-0.196	0.892	0.075	0.083	0.144	49
		soil water content in samples	% g^{-1} soil DM	-27.109	33.061	15.099	14.479	10.607	50
		ammonium	µg N g^{-1} soil DM	-35.54	18.723	-5.487	-6.23	10.187	50
		nitrate	µg N g^{-1} soil DM	-38.008	14.17	-7.204	-8.619	10.277	50
		Nmin	µg N g^{-1} soil DM	-39.304	14.075	-16.569	-14.849	12.848	50
		Cmic:Ct ratio		-1.898	3.613	0.239	0.164	1.277	49
		C:N ratio		-0.743	0.531	0.009	-0.011	0.176	50
		EOC	µg C g^{-1} soil DM	-100.093	192.881	40.008	48.423	71.678	50
		EN	µg N g^{-1} soil DM	-22.174	22.931	-2.661	-2.832	8.802	50

Table S4 continued

		Variable	Unit	min	max	Central median	mean	SD	N
response variable (change between 2011 and 2014)	microbial biomass	Cmic	µg C g^{-1} soil DM	-219.45	145.68	-43.10	-42.74	82.19	50
		Nmic	µg N g^{-1} soil DM	-68.30	17.58	-15.90	-16.91	17.32	50
		Cmic:Nmic ratio		-0.66	2.71	0.66	0.76	0.78	50
		Pmic	µg P g^{-1} soil DM	-44.05	51.55	-6.96	-6.16	21.19	45
	enzyme activiy	beta-glucosidase	nmol MUF g^{-1} h^{-1}	-914.27	1075.71	25.36	32.09	326.06	50
		beta-xylosidase	nmol MUF g^{-1} h^{-1}	-251.36	269.24	28.56	32.37	84.58	48
		chitinase	nmol MUF g^{-1} h^{-1}	-291.36	477.41	85.82	100.20	130.90	50
		urease	µg N g^{-1} DM 2h^{-1}	-224.06	39.28	-39.27	-42.49	62.81	45
		DEA	µg N_2O-N + N_2-N g^{-1} soil DM h^{-1}	-1.32	2.47	0.34	0.34	0.60	50
		phosphatase	nmol MUF g^{-1} h^{-1}	-579.22	874.99	101.98	73.69	244.47	50
	microbial community	bacteria	nmol FAME g^{-1} soil DM	-38.91	48.68	-2.35	-0.92	18.55	50
		gram negative bacteria	nmol FAME g^{-1} soil DM	-3.89	8.33	1.48	1.82	2.92	50
		gram positive bacteria	nmol FAME g^{-1} soil DM	-28.64	30.31	-1.20	-1.89	11.31	50
		fungi	nmol FAME g^{-1} soil DM	-4.50	5.60	2.00	2.09	2.16	50
		fungi:bacteria ratio		-0.02	0.12	0.03	0.04	0.03	50
		ergosterol	µg g^{-1} soil DM	-7.09	8.42	1.36	1.37	3.44	47
		invertebrates	nmol FAME g^{-1} soil DM	-0.95	1.91	0.08	0.20	0.55	50
		sum microbial PLFA	nmol FAME g^{-1} soil DM	-0.53	142.63	50.11	56.28	33.37	50
explanatory variables	abiotic factors	temperature change	°C	-1.91	9.80	0.17	0.39	1.61	48
		soil water content change	% vol. of water holding capacity	-10.20	22.97	5.46	4.92	6.01	49
		pH change	in $CaCl_2$	-0.28	0.31	-0.11	-0.08	0.12	50
		pH historic	in $CaCl_2$	5.02	7.45	7.09	6.89	0.51	50
	land-use intensity	LUI change	dimensionless	-0.77	1.21	-0.06	-0.02	0.40	50
		LUI historic	dimensionless	0.63	3.05	1.67	1.62	0.63	50
		mowing change	no. of cuts per year	-2.23	0.96	0.00	0.00	0.63	50
		fertilization change	kg N ha^{-1} a^{-1}	-2.81	3.05	0.00	0.00	1.05	50
		grazing change	livestock units d ha^{-1} year^{-1}	-2.81	6.56	-0.11	0.00	1.28	50
	plant functional traits	CWM MycInt change	% colonized root length	-24.73	14.05	0.79	0.10	7.11	50
		CWM MycInt historic	% colonized root length	39.72	58.53	52.23	51.43	4.36	50
		CWM SLA change	mm² g^{-1} DM	-4.41	3.95	0.23	0.37	1.53	50
		CWM SLA historic	mm² g^{-1} DM	21.61	29.51	26.37	25.95	1.88	50
		CWM leaf P change	mg P g^{-1} DM	-0.90	1.81	-0.12	-0.10	0.41	50
		CWM leaf P historic	mg P g^{-1} DM	1.73	3.67	2.60	2.59	0.42	50
		CWM leaf N change	mg N g^{-1} DM	-7.72	4.20	-0.12	-0.11	2.49	50
		CWM leaf N historic	mg N g^{-1} DM	21.17	31.92	28.30	28.38	2.79	50

Table S4 continued

		Variable	Unit	min	max	Central median	mean	SD	N
explanatory variables	plant biomass properties	plant biomass change	g m^{-2}	-53.55	391.30	157.50	162.98	96.34	50
		plant biomass cellulose content change	%	-0.48	9.83	3.20	3.70	2.29	50
		plant biomass hemicelluloses content change	%	-10.53	11.58	-0.03	0.19	5.72	50
		plant biomass lignin content change	%	-1.82	3.92	0.63	0.67	1.30	50
		plant biomass lignin:N ratio change		-0.78	2.59	0.61	0.63	0.75	50
		plant biomass N content change	%	-1.21	0.63	-0.19	-0.22	0.38	50
		plant biomass P content change	%	-0.06	0.15	0.06	0.05	0.04	50
	excluded	fast-slow gradient change	site scores PC1	-3.70	3.61	-0.43	-0.21	1.52	50
		fast-slow gradient historic	site scores PC1	-2.67	3.29	0.15	0.16	1.46	50
		Rao's Q change	index	-0.01	0.01	0.00	0.00	0.00	50
		Rao's Q historic	index	0.01	0.02	0.02	0.02	0.00	50
		number of species change	count	-5.00	15.00	3.00	3.50	4.95	50
		number of species historic	count	13.25	61.75	27.88	29.81	10.80	50
		number of grasses change	count	-4.00	4.00	1.00	0.52	1.99	50
		number of herbs change	count	-4.00	10.00	3.00	2.84	3.44	50
		number of legumes change	count	-3.00	3.00	0.00	0.02	1.35	50
background variables (change between 2011 and 2014)		bulk density	g cm^{-3}	-0.274	0.39	0.068	0.066	0.108	47
		soil water content in samples	% g^{-1} soil DM	1.227	25.734	11.06	10.952	6.013	50
		ammonium	µg N g^{-1} soil DM	-6.891	23.306	3.589	3.906	5.931	50
		nitrate	µg N g^{-1} soil DM	-23.667	33.505	-2.33	0.032	12.095	50
		Nmin	µg N g^{-1} soil DM	-30.558	32.546	2.242	3.938	13.164	50
		Cmic:Ct ratio		-2.319	6.67	1.316	1.287	1.69	50
		C:N ratio		-0.895	0.274	-0.125	-0.201	0.255	50
		EOC	µg C g^{-1} soil DM	-147.669	119.939	-14.975	-24.206	57.62	50
		EN	µg N g^{-1} soil DM	-32.6	32.653	3.578	3.519	10.755	50

Table S4 continued

		Variable	Unit	North-East					
				min	max	median	mean	SD	N
response variable (change between 2011 and 2014)	microbial biomass	Cmic	µg C g^{-1} soil DM	-362.66	224.35	-54.55	-67.48	118.44	50
		Nmic	µg N g^{-1} soil DM	-67.22	62.88	-4.73	-2.87	25.63	50
		Cmic:Nmic ratio		-2.89	1.84	-0.45	-0.43	0.79	50
		Pmic	µg P g^{-1} soil DM	-39.51	51.01	-8.18	-2.25	20.39	46
	enzyme activiy	beta-glucosidase	nmol MUF g^{-1} h^{-1}	-990.61	1434.12	96.29	190.09	511.64	50
		beta-xylosidase	nmol MUF g^{-1} h^{-1}	-108.24	386.74	47.73	77.15	97.49	50
		chitinase	nmol MUF g^{-1} h^{-1}	-261.82	711.18	94.03	126.78	184.53	50
		urease	µg N g^{-1} DM 2h^{-1}	-201.71	347.94	34.72	63.41	99.62	50
		DEA	µg N_2O-N + N_2-N g^{-1} soil DM h^{-1}	-0.26	4.99	1.38	1.43	1.21	50
		phosphatase	nmol MUF g^{-1} h^{-1}	-1043.77	5400.01	344.25	530.56	897.41	50
	microbial community	bacteria	nmol FAME g^{-1} soil DM	-82.71	43.32	4.93	2.46	23.17	50
		gram negative bacteria	nmol FAME g^{-1} soil DM	-10.14	7.24	-0.39	-0.16	2.97	50
		gram positive bacteria	nmol FAME g^{-1} soil DM	-47.80	28.71	3.84	1.59	14.19	50
		fungi	nmol FAME g^{-1} soil DM	-2.93	4.15	0.38	0.31	1.19	50
		fungi:bacteria ratio		-0.04	0.08	0.00	0.00	0.02	50
		ergosterol	µg g^{-1} soil DM	-6.78	24.62	1.56	2.04	4.57	50
		invertebrates	nmol FAME g^{-1} soil DM	-1.00	1.14	-0.08	-0.03	0.49	50
		sum microbial PLFA	nmol FAME g^{-1} soil DM	-63.58	150.52	36.14	50.72	43.28	50
explanatory variables	abiotic factors	temperature change	°C	-0.33	8.90	1.16	1.57	1.75	50
		soil water content change	% vol. of water holding capacity	-18.87	47.22	3.56	4.57	9.89	50
		pH change	in $CaCl_2$	-1.64	1.39	-0.09	0.00	0.37	50
		pH historic	in $CaCl_2$	4.58	7.43	6.43	6.39	0.91	50
	land-use intensity	LUI change	dimensionless	-2.02	2.72	0.06	-0.04	0.81	50
		LUI historic	dimensionless	0.92	2.93	1.40	1.63	0.58	50
		mowing change	no. of cuts per year	-1.06	2.38	0.00	0.00	0.74	50
		fertilization change	kg N ha^{-1} a^{-1}	-7.96	13.65	0.00	0.00	3.82	50
		grazing change	livestock units d ha^{-1} year^{-1}	-2.91	2.42	0.00	0.00	0.90	50
	plant functional traits	CWM MycInt change	% colonized root length	-29.46	15.99	2.67	0.29	8.33	50
		CWM MycInt historic	% colonized root length	27.45	67.58	49.48	48.80	7.79	50
		CWM SLA change	mm² g^{-1} DM	-5.05	5.03	0.41	0.56	1.84	50
		CWM SLA historic	mm² g^{-1} DM	23.06	31.11	27.48	27.45	1.89	50
		CWM leaf P change	mg P g^{-1} DM	-1.33	0.88	-0.15	-0.12	0.47	50
		CWM leaf P historic	mg P g^{-1} DM	2.18	4.20	2.92	2.94	0.43	50
		CWM leaf N change	mg N g^{-1} DM	-6.68	7.93	1.47	1.01	2.53	50
		CWM leaf N historic	mg N g^{-1} DM	22.32	35.15	29.31	29.04	2.51	50

Table S4 continued

		Variable	Unit	North-East					
				min	max	median	mean	SD	N
explanatory variables	plant biomass properties	plant biomass change	g m^{-2}	-81.55	611.85	173.75	174.82	157.66	49
		plant biomass cellulose content change	%	-3.54	10.07	1.85	2.12	2.55	49
		plant biomass hemicelluloses content change	%	-12.38	16.38	1.88	2.08	6.14	49
		plant biomass lignin content change	%	-2.59	2.98	0.88	0.72	1.26	49
		plant biomass lignin:N ratio change		-1.50	2.63	0.35	0.38	0.64	49
		plant biomass N content change	%	-1.26	1.39	-0.06	-0.05	0.55	49
		plant biomass P content change	%	-0.03	0.19	0.07	0.07	0.05	49
	excluded	fast-slow gradient change	site scores PC1	-2.96	4.36	0.21	0.39	1.56	50
		fast-slow gradient historic	site scores PC1	-3.13	2.86	-0.93	-0.74	1.38	50
		Rao's Q change	index	-0.01	0.01	0.00	0.00	0.00	50
		Rao's Q historic	index	0.01	0.03	0.02	0.02	0.00	50
		number of species change	count	-6.00	10.00	3.00	2.12	3.76	50
		number of species historic	count	13.00	27.25	19.00	19.20	3.45	50
		number of grasses change	count	-2.00	5.00	1.00	1.08	1.28	50
		number of herbs change	count	-6.00	5.00	0.00	0.16	2.74	50
		number of legumes change	count	-1.00	4.00	0.00	0.72	1.23	50
background variables (change between 2011 and 2014)		bulk density	g cm^{-3}	-0.166	0.33	0.069	0.073	0.098	50
		soil water content in samples	% g^{-1} soil DM	-15.16	28.367	7.054	7.136	7.7	50
		ammonium	µg N g^{-1} soil DM	-37.128	71.748	-1.612	-3.64	14.582	50
		nitrate	µg N g^{-1} soil DM	-30.739	73.36	0.408	4.132	18.193	50
		Nmin	µg N g^{-1} soil DM	-54.85	90.635	1.92	0.492	23.156	50
		Cmic:Ct ratio		-4.728	1.565	-0.818	-0.973	1.352	50
		C:N ratio		-0.824	1.545	-0.053	-0.067	0.337	50
		EOC	µg C g^{-1} soil DM	-335.436	223.978	-10.903	-23.174	96.42	50
		EN	µg N g^{-1} soil DM	-90.64	110.188	2.206	-1.054	23.351	50

Table S5: Hierarchical levels of multiple regression analyses (Δ = change, h = historic, bv = background value).

Level	**overall description**	**fixed effects**
Level 1	abiotic factors I	Δtemperature, Δsoil water content, pH_{bv}
Level 2	land-use intensity	LUI_h, ΔLUI
Level 3	abiotic factors II	ΔpH
Level 4	plant functional traits	ΔCWM MycInt, CWM $MycInt_h$, ΔCWM SLA, CWM SLA_h, ΔCWM leaf P, CWM leaf P_h, ΔCWM leaf N, CWM leaf N_h
Level 5	plant biomass properties	Δplant biomass, Δplant biomass cellulose content, Δplant biomass hemicelluloses content, Δplant biomass lignin content, Δplant biomass P content, Δplant biomass N content, Δplant biomass

Table S6.1: Model fits of SEMs in Schwäbische Alb (South-West), Hainich-Dün (Central) and Schorfheide-Chorin (North-East). Given are the model fit values for the five tested mediator types. Insignificant *p*-value of X^2 were highlighted in green and the model with the lowest AIC value in red. If the model with the lowest AIC value had a significant *p*-value of X^2, the model with the next lower AIC without a significant *p*-value of X^2 was chosen (according to the t-rule model fit based on chi-square tests could not be assessed for SEMs with plant biomass and lignin). ntotal = no. of samples, npar = no. of estimated parameters, df = degrees of freedom, *p* = *p*-value of X^2, rmsea = root means square error, rmsea.*p* = *p*-value of rmsea, AIC = Akaike's information criterion, O2E = ratio of observed samples:estimated parameters.

Region	**MO variable**	**mediator**	**ntotal**	**npar**	**X^2**	**df**	***p***	**rmsea**	**rmsea.*p***	**AIC**	**O2E**
South-West	Cmic	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-87.31	4.00
South-West	Cmic	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-69.40	4.00
South-West	Cmic	Plant biomass	50	10	0.00	0	NA	0.00	NA	-55.85	5.00
South-West	Cmic	Lignin content	48	10	0.00	0	NA	0.00	NA	-26.80	4.80
South-West	Cmic	pH	50	12	8.72	3	0.03	0.20	0.05	-53.84	4.17
South-West	Nmic	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-95.16	4.00
South-West	Nmic	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-77.16	4.00
South-West	Nmic	Plant biomass	50	10	0.00	0	NA	0.00	NA	-63.13	5.00
South-West	Nmic	Lignin content	48	10	0.00	0	NA	0.00	NA	-35.05	4.80
South-West	Nmic	pH	50	12	8.72	3	0.03	0.20	0.05	-62.97	4.17
South-West	Cmic:Nmic ratio	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-73.08	4.00
South-West	Cmic:Nmic ratio	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-55.48	4.00
South-West	Cmic:Nmic ratio	Plant biomass	50	10	0.00	0	NA	0.00	NA	-36.64	5.00
South-West	Cmic:Nmic ratio	Lignin content	48	10	0.00	0	NA	0.00	NA	-15.55	4.80
South-West	Cmic:Nmic ratio	pH	50	12	8.72	3	0.03	0.20	0.05	-41.39	4.17
South-West	Pmic	**CWM leaf P**	37	12	4.66	3	0.20	0.12	0.23	-68.98	3.08
South-West	Pmic	CWM MycInt	37	12	10.53	3	0.01	0.26	0.02	-63.40	3.08
South-West	Pmic	Plant biomass	39	10	0.00	0	NA	0.00	NA	-28.16	3.90
South-West	Pmic	Lignin content	37	10	0.00	0	NA	0.00	NA	-11.24	3.70
South-West	Pmic	pH	39	12	9.99	3	0.02	0.24	0.03	-39.02	3.25
South-West	glucosidase	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-85.80	4.00
South-West	glucosidase	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-59.94	4.00
South-West	glucosidase	Plant biomass	50	10	0.00	0	NA	0.00	NA	-42.10	5.00
South-West	glucosidase	Lignin content	48	10	0.00	0	NA	0.00	NA	-20.73	4.80
South-West	glucosidase	pH	50	12	8.72	3	0.03	0.20	0.05	-48.66	4.17
South-West	xylosidase	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-90.09	4.00
South-West	xylosidase	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-65.13	4.00
South-West	xylosidase	Plant biomass	50	10	0.00	0	NA	0.00	NA	-47.35	5.00
South-West	xylosidase	Lignin content	48	10	0.00	0	NA	0.00	NA	-27.28	4.80
South-West	xylosidase	pH	50	12	8.72	3	0.03	0.20	0.05	-61.12	4.17
South-West	chitinase	**CWM leaf P**	45	12	4.56	3	0.21	0.11	0.25	-96.19	3.75
South-West	chitinase	CWM MycInt	45	12	9.53	3	0.02	0.22	0.04	-67.27	3.75
South-West	chitinase	Plant biomass	47	10	0.00	0	NA	0.00	NA	-49.85	4.70
South-West	chitinase	Lignin content	45	10	0.00	0	NA	0.00	NA	-30.85	4.50
South-West	chitinase	pH	47	12	7.58	3	0.06	0.18	0.08	-54.12	3.92

Table S6.1 continued

Region	MO variable	mediator	ntotal	npar	X^2	df	*p*	rmsea	rmsea.*p*	AIC	O2E
South-West	urease	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-95.58	4.00
South-West	urease	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-77.49	4.00
South-West	urease	Plant biomass	50	10	0.00	0	NA	0.00	NA	-51.71	5.00
South-West	urease	Lignin content	48	10	0.00	0	NA	0.00	NA	-31.69	4.80
South-West	urease	pH	50	12	8.72	3	0.03	0.20	0.05	-54.52	4.17
South-West	DEA	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-106.19	4.00
South-West	DEA	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-79.51	4.00
South-West	DEA	Plant biomass	50	10	0.00	0	NA	0.00	NA	-61.14	5.00
South-West	DEA	Lignin content	48	10	0.00	0	NA	0.00	NA	-40.52	4.80
South-West	DEA	pH	50	12	8.72	3	0.03	0.20	0.05	-66.45	4.17
South-West	phosphatase	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-83.60	4.00
South-West	phosphatase	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-65.88	4.00
South-West	phosphatase	Plant biomass	50	10	0.00	0	NA	0.00	NA	-46.12	5.00
South-West	phosphatase	Lignin content	48	10	0.00	0	NA	0.00	NA	-32.41	4.80
South-West	phosphatase	pH	50	12	8.72	3	0.03	0.20	0.05	-88.18	4.17
South-West	bacteria	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-85.92	4.00
South-West	bacteria	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-69.58	4.00
South-West	bacteria	Plant biomass	50	10	0.00	0	NA	0.00	NA	-48.27	5.00
South-West	bacteria	Lignin content	48	10	0.00	0	NA	0.00	NA	-27.34	4.80
South-West	bacteria	pH	50	12	8.72	3	0.03	0.20	0.05	-56.77	4.17
South-West	fungi	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-87.28	4.00
South-West	fungi	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-68.65	4.00
South-West	fungi	Plant biomass	50	10	0.00	0	NA	0.00	NA	-48.45	5.00
South-West	fungi	Lignin content	48	10	0.00	0	NA	0.00	NA	-27.44	4.80
South-West	fungi	pH	50	12	8.72	3	0.03	0.20	0.05	-52.31	4.17
South-West	fungi:bacteria rati	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-84.02	4.00
South-West	fungi:bacteria rati	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-60.38	4.00
South-West	fungi:bacteria rati	Plant biomass	50	10	0.00	0	NA	0.00	NA	-41.75	5.00
South-West	fungi:bacteria rati	Lignin content	48	10	0.00	0	NA	0.00	NA	-22.01	4.80
South-West	fungi:bacteria rati	pH	50	12	8.72	3	0.03	0.20	0.05	-49.09	4.17
South-West	ergosterol	**CWM leaf P**	48	12	6.31	3	0.10	0.15	0.13	-82.95	4.00
South-West	ergosterol	CWM MycInt	48	12	9.23	3	0.03	0.21	0.04	-62.80	4.00
South-West	ergosterol	Plant biomass	50	10	0.00	0	NA	0.00	NA	-38.99	5.00
South-West	ergosterol	Lignin content	48	10	0.00	0	NA	0.00	NA	-19.77	4.80
South-West	ergosterol	pH	50	12	8.72	3	0.03	0.20	0.05	-43.20	4.17
Central	Cmic	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-89.13	4.17
Central	Cmic	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-38.43	4.17
Central	Cmic	Plant biomass	50	10	0.00	0	NA	0.00	NA	-19.96	5.00
Central	Cmic	Lignin content	50	10	0.00	0	NA	0.00	NA	-14.50	5.00
Central	Cmic	pH	50	12	21.62	3	0.00	0.35	0.00	-34.42	4.17
Central	Nmic	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-107.87	4.17
Central	Nmic	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-57.19	4.17
Central	Nmic	Plant biomass	50	10	0.00	0	NA	0.00	NA	-37.91	5.00
Central	Nmic	Lignin content	50	10	0.00	0	NA	0.00	NA	-33.75	5.00
Central	Nmic	pH	50	12	21.62	3	0.00	0.35	0.00	-51.88	4.17

Table S6.1 continued

Region	**MO variable**	**mediator**	**ntotal**	**npar**	**X^2**	**df**	***p***	**rmsea**	**rmsea.*p***	**AIC**	**O2E**
Central	Cmic:Nmic ratio	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-87.70	4.17
Central	Cmic:Nmic ratio	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-37.50	4.17
Central	Cmic:Nmic ratio	Plant biomass	50	10	0.00	0	NA	0.00	NA	-19.42	5.00
Central	Cmic:Nmic ratio	Lignin content	50	10	0.00	0	NA	0.00	NA	-13.81	5.00
Central	Cmic:Nmic ratio	pH	50	12	21.62	3	0.00	0.35	0.00	-41.14	4.17
Central	Pmic	**CWM leaf P**	45	12	6.36	3	0.10	0.16	0.13	-75.18	3.75
Central	Pmic	CWM MycInt	45	12	9.61	3	0.02	0.22	0.03	-19.27	3.75
Central	Pmic	Plant biomass	45	10	0.00	0	NA	0.00	NA	-7.63	4.50
Central	Pmic	Lignin content	45	10	0.00	0	NA	0.00	NA	-3.07	4.50
Central	Pmic	pH	45	12	20.04	3	0.00	0.36	0.00	-19.06	3.75
Central	glucosidase	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-138.60	4.17
Central	glucosidase	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-72.80	4.17
Central	glucosidase	Plant biomass	50	10	0.00	0	NA	0.00	NA	-55.60	5.00
Central	glucosidase	Lignin content	50	10	0.00	0	NA	0.00	NA	-47.83	5.00
Central	glucosidase	pH	50	12	21.62	3	0.00	0.35	0.00	-66.96	4.17
Central	xylosidase	**CWM leaf P**	48	12	3.01	3	0.39	0.01	0.44	-127.99	4.00
Central	xylosidase	CWM MycInt	48	12	7.66	3	0.05	0.18	0.08	-72.95	4.00
Central	xylosidase	Plant biomass	48	10	0.00	0	NA	0.00	NA	-57.10	4.80
Central	xylosidase	Lignin content	48	10	0.00	0	NA	0.00	NA	-51.30	4.80
Central	xylosidase	pH	48	12	21.35	3	0.00	0.36	0.00	-65.43	4.00
Central	chitinase	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-126.86	4.17
Central	chitinase	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-67.61	4.17
Central	chitinase	Plant biomass	50	10	0.00	0	NA	0.00	NA	-51.47	5.00
Central	chitinase	Lignin content	50	10	0.00	0	NA	0.00	NA	-49.09	5.00
Central	chitinase	pH	50	12	21.62	3	0.00	0.35	0.00	-64.59	4.17
Central	urease	**CWM leaf P**	45	12	3.84	3	0.28	0.08	0.33	-72.35	3.75
Central	urease	CWM MycInt	45	12	12.33	3	0.01	0.26	0.01	-22.51	3.75
Central	urease	Plant biomass	45	10	0.00	0	NA	0.00	NA	-10.71	4.50
Central	urease	Lignin content	45	10	0.00	0	NA	0.00	NA	-12.25	4.50
Central	urease	pH	45	12	18.53	3	0.00	0.34	0.00	-21.60	3.75
Central	DEA	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-125.66	4.17
Central	DEA	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-73.03	4.17
Central	DEA	Plant biomass	50	10	0.00	0	NA	0.00	NA	-68.20	5.00
Central	DEA	Lignin content	50	10	0.00	0	NA	0.00	NA	-50.68	5.00
Central	DEA	pH	50	12	21.62	3	0.00	0.35	0.00	-69.63	4.17
Central	phosphatase	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-121.60	4.17
Central	phosphatase	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-67.66	4.17
Central	phosphatase	Plant biomass	50	10	0.00	0	NA	0.00	NA	-52.26	5.00
Central	phosphatase	Lignin content	50	10	0.00	0	NA	0.00	NA	-46.22	5.00
Central	phosphatase	pH	50	12	21.62	3	0.00	0.35	0.00	-67.40	4.17
Central	bacteria	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-92.75	4.17
Central	bacteria	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-50.43	4.17
Central	bacteria	Plant biomass	50	10	0.00	0	NA	0.00	NA	-32.84	5.00
Central	bacteria	Lignin content	50	10	0.00	0	NA	0.00	NA	-19.43	5.00
Central	bacteria	pH	50	12	21.62	3	0.00	0.35	0.00	-40.09	4.17

Table S6.1 continued

Region	MO variable	mediator	ntotal	npar	X^2	df	*p*	rmsea	rmsea.*p*	AIC	O2E
Central	fungi	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-97.14	4.17
Central	fungi	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-49.11	4.17
Central	fungi	Plant biomass	50	10	0.00	0	NA	0.00	NA	-30.82	5.00
Central	fungi	Lignin content	50	10	0.00	0	NA	0.00	NA	-23.52	5.00
Central	fungi	pH	50	12	21.62	3	0.00	0.35	0.00	-44.62	4.17
Central	fungi:bacteria rati	**CWM leaf P**	50	12	3.44	3	0.33	0.05	0.38	-98.91	4.17
Central	fungi:bacteria rati	CWM MycInt	50	12	9.29	3	0.03	0.20	0.04	-48.74	4.17
Central	fungi:bacteria rati	Plant biomass	50	10	0.00	0	NA	0.00	NA	-30.68	5.00
Central	fungi:bacteria rati	Lignin content	50	10	0.00	0	NA	0.00	NA	-25.76	5.00
Central	fungi:bacteria rati	pH	50	12	21.62	3	0.00	0.35	0.00	-43.98	4.17
Central	ergosterol	**CWM leaf P**	47	12	3.53	3	0.32	0.06	0.37	-76.15	3.92
Central	ergosterol	CWM MycInt	47	12	10.12	3	0.02	0.22	0.03	-31.86	3.92
Central	ergosterol	Plant biomass	47	10	0.00	0	NA	0.00	NA	-16.24	4.70
Central	ergosterol	Lignin content	47	10	0.00	0	NA	0.00	NA	-13.43	4.70
Central	ergosterol	pH	47	12	24.77	3	0.00	0.39	0.00	-31.19	3.92
North-East	Cmic	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-54.46	4.17
North-East	Cmic	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-84.56	4.17
North-East	Cmic	Plant biomass	49	10	0.00	0	NA	0.00	NA	-44.38	4.90
North-East	Cmic	Lignin content	49	10	0.00	0	NA	0.00	NA	-35.53	4.90
North-East	Cmic	pH	50	12	11.30	3	0.01	0.24	0.02	-71.18	4.17
North-East	Nmic	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-56.68	4.17
North-East	Nmic	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-82.74	4.17
North-East	Nmic	Plant biomass	49	10	0.00	0	NA	0.00	NA	-43.18	4.90
North-East	Nmic	Lignin content	49	10	0.00	0	NA	0.00	NA	-37.43	4.90
North-East	Nmic	pH	50	12	11.30	3	0.01	0.24	0.02	-74.08	4.17
North-East	Cmic:Nmic ratio	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-78.91	4.17
North-East	Cmic:Nmic ratio	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-103.35	4.17
North-East	Cmic:Nmic ratio	Plant biomass	49	10	0.00	0	NA	0.00	NA	-60.00	4.90
North-East	Cmic:Nmic ratio	Lignin content	49	10	0.00	0	NA	0.00	NA	-57.93	4.90
North-East	Cmic:Nmic ratio	pH	50	12	11.30	3	0.01	0.24	0.02	-106.48	4.17
North-East	Pmic	CWM leaf P	46	12	24.31	3	0.00	0.39	0.00	-44.22	3.83
North-East	Pmic	CWM MycInt	46	12	28.49	3	0.00	0.43	0.00	-73.97	3.83
North-East	Pmic	Plant biomass	45	10	0.00	0	NA	0.00	NA	-24.47	4.50
North-East	Pmic	Lignin content	45	10	0.00	0	NA	0.00	NA	-25.38	4.50
North-East	Pmic	pH	46	12	10.01	3	0.02	0.23	0.03	-49.69	3.83
North-East	glucosidase	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-51.42	4.17
North-East	glucosidase	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-81.07	4.17
North-East	glucosidase	Plant biomass	49	10	0.00	0	NA	0.00	NA	-32.03	4.90
North-East	glucosidase	Lignin content	49	10	0.00	0	NA	0.00	NA	-32.96	4.90
North-East	glucosidase	pH	50	12	11.30	3	0.01	0.24	0.02	-82.23	4.17
North-East	xylosidase	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-59.46	4.17
North-East	xylosidase	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-89.46	4.17
North-East	xylosidase	Plant biomass	49	10	0.00	0	NA	0.00	NA	-39.67	4.90
North-East	xylosidase	Lignin content	49	10	0.00	0	NA	0.00	NA	-40.48	4.90
North-East	xylosidase	pH	50	12	11.30	3	0.01	0.24	0.02	-80.28	4.17

Table S6.1 continued

Region	MO variable	mediator	ntotal	npar	X^2	df	*p*	rmsea	rmsea.*p*	AIC	O2E
North-East	chitinase	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-66.37	4.17
North-East	chitinase	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-91.19	4.17
North-East	chitinase	Plant biomass	49	10	0.00	0	NA	0.00	NA	-44.14	4.90
North-East	chitinase	Lignin content	49	10	0.00	0	NA	0.00	NA	-44.90	4.90
North-East	chitinase	pH	50	12	11.30	3	0.01	0.24	0.02	-82.26	4.17
North-East	urease	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-66.09	4.17
North-East	urease	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-94.64	4.17
North-East	urease	Plant biomass	49	10	0.00	0	NA	0.00	NA	-45.81	4.90
North-East	urease	Lignin content	49	10	0.00	0	NA	0.00	NA	-46.62	4.90
North-East	urease	pH	50	12	11.30	3	0.01	0.24	0.02	-101.17	4.17
North-East	DEA	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-45.36	4.17
North-East	DEA	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-75.05	4.17
North-East	DEA	Plant biomass	49	10	0.00	0	NA	0.00	NA	-22.60	4.90
North-East	DEA	Lignin content	49	10	0.00	0	NA	0.00	NA	-23.22	4.90
North-East	DEA	pH	50	12	11.30	3	0.01	0.24	0.02	-79.56	4.17
North-East	phosphatase	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-103.75	4.17
North-East	phosphatase	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-124.61	4.17
North-East	phosphatase	Plant biomass	49	10	0.00	0	NA	0.00	NA	-77.17	4.90
North-East	phosphatase	Lignin content	49	10	0.00	0	NA	0.00	NA	-77.95	4.90
North-East	phosphatase	pH	50	12	11.30	3	0.01	0.24	0.02	-117.55	4.17
North-East	bacteria	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-68.04	4.17
North-East	bacteria	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-99.86	4.17
North-East	bacteria	Plant biomass	49	10	0.00	0	NA	0.00	NA	-48.55	4.90
North-East	bacteria	Lignin content	49	10	0.00	0	NA	0.00	NA	-46.73	4.90
North-East	bacteria	pH	50	12	11.30	3	0.01	0.24	0.02	-79.94	4.17
North-East	fungi	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-77.01	4.17
North-East	fungi	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-109.60	4.17
North-East	fungi	Plant biomass	49	10	0.00	0	NA	0.00	NA	-57.28	4.90
North-East	fungi	Lignin content	49	10	0.00	0	NA	0.00	NA	-57.83	4.90
North-East	fungi	pH	50	12	11.30	3	0.01	0.24	0.02	-91.74	4.17
North-East	fungi:bacteria rati	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-76.56	4.17
North-East	fungi:bacteria rati	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-100.54	4.17
North-East	fungi:bacteria rati	Plant biomass	49	10	0.00	0	NA	0.00	NA	-59.57	4.90
North-East	fungi:bacteria rati	Lignin content	49	10	0.00	0	NA	0.00	NA	-60.89	4.90
North-East	fungi:bacteria rati	pH	50	12	11.30	3	0.01	0.24	0.02	-89.50	4.17
North-East	ergosterol	CWM leaf P	50	12	27.36	3	0.00	0.40	0.00	-95.11	4.17
North-East	ergosterol	CWM MycInt	50	12	29.64	3	0.00	0.42	0.00	-119.49	4.17
North-East	ergosterol	Plant biomass	49	10	0.00	0	NA	0.00	NA	-79.02	4.90
North-East	ergosterol	Lignin content	49	10	0.00	0	NA	0.00	NA	-74.93	4.90
North-East	ergosterol	pH	50	12	11.30	3	0.01	0.24	0.02	-121.36	4.17

Table S6.2: Estimates of SEMs in Schwäbische Alb (South-West), Hainich-Dün (Central) and Schorfheide-Chorin (North-East). Given are the unstandardized regression coefficients (est) with their standard error (se), z-value (z) and respective *p*-value (*p*), as well as the standardized correlation coefficients (est.std) with their standard error (se.std), z-value (z.std) and *p*-value (*p*.std) for each microbial variable (MO variable) and the five selected mediator variables (mediator). The single model paths are described by lhs = left hand side, op = operator, rhs = right hand side and if applicable the respective label of the path.

Region	**MO variable**	**mediator**	**lhs**	**op**	**rhs**	**label**	**est**	**se**	**z**	***p***	**est.std**	**se.std**	**z.std**	***p*.std**
South-West	Cmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	Cmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	Cmic	CWM_leaf_P	Cmic	~	CWM_leafP_historic	c	0.03	0.15	0.18	0.854	0.04	0.20	0.18	0.854
South-West	Cmic	CWM_leaf_P	Cmic	~	CWM_leafP_change	d	0.35	0.16	2.20	0.028	0.30	0.13	2.29	0.022
South-West	Cmic	CWM_leaf_P	Cmic	~	LUI_historic	e	0.12	0.22	0.54	0.592	0.11	0.20	0.54	0.591
South-West	Cmic	CWM_leaf_P	Cmic	~	LUI_change	f	-0.12	0.13	-0.95	0.341	-0.13	0.14	-0.96	0.337
South-West	Cmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	Cmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	Cmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	Cmic	CWM_leaf_P	Cmic	~~	Cmic		0.04	0.01	4.90	0.000	0.88	0.09	10.04	0.000
South-West	Cmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.16	0.18	0.855	0.03	0.14	0.18	0.855
South-West	Cmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.55	0.583	0.02	0.04	0.55	0.583
South-West	Cmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.15	0.15	0.96	0.336	0.13	0.14	0.97	0.333
South-West	Cmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.10	0.13	-0.74	0.458	-0.11	0.14	-0.75	0.456
South-West	Cmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.15	0.15	0.97	0.335	0.14	0.14	1.06	0.289
South-West	Cmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.13	-0.75	0.455	-0.12	0.14	-0.85	0.394
South-West	Cmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	Cmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	Cmic	CWM_MycInt	Cmic	~	CWM_MycInt_historic	c	0.04	0.12	0.30	0.761	0.04	0.14	0.30	0.761
South-West	Cmic	CWM_MycInt	Cmic	~	CWM_MycInt_change	d	0.39	0.17	2.37	0.018	0.33	0.13	2.49	0.013
South-West	Cmic	CWM_MycInt	Cmic	~	LUI_historic	e	0.21	0.16	1.34	0.180	0.19	0.14	1.36	0.174
South-West	Cmic	CWM_MycInt	Cmic	~	LUI_change	f	-0.18	0.13	-1.37	0.170	-0.19	0.14	-1.39	0.164
South-West	Cmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	Cmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	Cmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	Cmic	CWM_MycInt	Cmic	~~	Cmic		0.04	0.01	4.90	0.000	0.85	0.09	8.96	0.000
South-West	Cmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.05	0.30	0.764	0.01	0.04	0.30	0.764
South-West	Cmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.09	0.06	1.61	0.108	0.10	0.06	1.63	0.104
South-West	Cmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.23	0.15	1.49	0.137	0.20	0.13	1.52	0.130
South-West	Cmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.09	0.13	-0.66	0.510	-0.09	0.14	-0.66	0.508
South-West	Cmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.23	0.15	1.49	0.136	0.21	0.13	1.60	0.109
South-West	Cmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.13	-0.67	0.504	-0.12	0.14	-0.82	0.415
South-West	Cmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	Cmic	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	Cmic	Plant_biomass	Cmic	~	Plant_biomass	c	0.39	0.12	3.14	0.002	0.40	0.12	3.41	0.001
South-West	Cmic	Plant_biomass	Cmic	~	LUI_historic	e	0.14	0.15	0.95	0.344	0.12	0.13	0.95	0.341
South-West	Cmic	Plant_biomass	Cmic	~	LUI_change	f	-0.10	0.11	-0.88	0.378	-0.11	0.13	-0.89	0.376
South-West	Cmic	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	Cmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	Cmic	Plant_biomass	Cmic	~~	Cmic		0.03	0.01	5.00	0.000	0.79	0.10	7.65	0.000
South-West	Cmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.07	0.07	1.09	0.274	0.07	0.06	1.11	0.266
South-West	Cmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.02	0.05	-0.29	0.772	-0.02	0.06	-0.29	0.771
South-West	Cmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.21	0.16	1.35	0.177	0.19	0.14	1.37	0.170
South-West	Cmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.11	0.12	-0.92	0.355	-0.13	0.14	-0.93	0.352
South-West	Cmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.21	0.16	1.36	0.175	0.21	0.14	1.52	0.128
South-West	Cmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.12	0.12	-0.94	0.349	-0.16	0.14	-1.13	0.259
South-West	Cmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	Cmic	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	Cmic	Lignin_content	Cmic	~	Lignin_content	c	0.11	0.12	0.90	0.368	0.13	0.14	0.91	0.364
South-West	Cmic	Lignin_content	Cmic	~	LUI_historic	e	0.21	0.16	1.33	0.183	0.19	0.14	1.35	0.176
South-West	Cmic	Lignin_content	Cmic	~	LUI_change	f	-0.12	0.12	-0.96	0.338	-0.14	0.14	-0.97	0.334
South-West	Cmic	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	Cmic	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	Cmic	Lignin_content	Cmic	~~	Cmic		0.04	0.01	4.90	0.000	0.93	0.07	12.77	0.000
South-West	Cmic	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.13	0.897	0.00	0.02	0.13	0.897
South-West	Cmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.46	0.643	0.01	0.02	0.46	0.643
South-West	Cmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.21	0.16	1.34	0.181	0.19	0.14	1.36	0.173
South-West	Cmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.11	0.13	-0.88	0.377	-0.13	0.14	-0.89	0.373
South-West	Cmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.22	0.16	1.34	0.179	0.21	0.14	1.49	0.135
South-West	Cmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.11	0.13	-0.90	0.371	-0.15	0.14	-1.07	0.284

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P*.std
South-West	Cmic	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	Cmic	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	Cmic	pH	Cmic	~	pH_historic	c	0.01	0.11	0.09	0.926	0.01	0.13	0.09	0.926
South-West	Cmic	pH	Cmic	~	pH_change	d	0.28	0.14	2.01	0.044	0.26	0.13	2.08	0.038
South-West	Cmic	pH	Cmic	~	LUI_historic	e	0.25	0.15	1.66	0.097	0.22	0.13	1.70	0.090
South-West	Cmic	pH	Cmic	~	LUI_change	f	-0.10	0.12	-0.87	0.387	-0.12	0.13	-0.87	0.384
South-West	Cmic	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	Cmic	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	Cmic	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	Cmic	pH	Cmic	~~	Cmic		0.04	0.01	5.00	0.000	0.86	0.09	9.58	0.000
South-West	Cmic	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.09	0.927	0.00	0.01	-0.09	0.927
South-West	Cmic	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.03	-0.08	0.933	0.00	0.04	-0.08	0.933
South-West	Cmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.25	0.15	1.66	0.097	0.22	0.13	1.69	0.090
South-West	Cmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.11	0.12	-0.86	0.392	-0.12	0.14	-0.86	0.389
South-West	Cmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.25	0.15	1.66	0.096	0.24	0.13	1.84	0.065
South-West	Cmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.11	0.12	-0.87	0.385	-0.15	0.14	-1.09	0.277
South-West	Nmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	Nmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	Nmic	CWM_leaf_P	Nmic	~	CWM_leafP_historic	c	0.00	0.14	-0.01	0.989	0.00	0.19	-0.01	0.989
South-West	Nmic	CWM_leaf_P	Nmic	~	CWM_leafP_change	d	0.31	0.15	2.10	0.036	0.28	0.13	2.18	0.029
South-West	Nmic	CWM_leaf_P	Nmic	~	LUI_historic	e	0.21	0.20	1.04	0.299	0.20	0.19	1.05	0.295
South-West	Nmic	CWM_leaf_P	Nmic	~	LUI_change	f	-0.13	0.12	-1.10	0.270	-0.15	0.13	-1.11	0.265
South-West	Nmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	Nmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	Nmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	Nmic	CWM_leaf_P	Nmic	~~	Nmic		0.03	0.01	4.90	0.000	0.86	0.09	9.35	0.000
South-West	Nmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Nmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Nmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.15	-0.01	0.989	0.00	0.14	-0.01	0.989
South-West	Nmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.55	0.584	0.02	0.04	0.55	0.584
South-West	Nmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.21	0.14	1.48	0.139	0.20	0.13	1.51	0.132
South-West	Nmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.11	0.12	-0.90	0.370	-0.13	0.14	-0.90	0.366
South-West	Nmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.21	0.14	1.49	0.137	0.21	0.13	1.62	0.105
South-West	Nmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.11	0.12	-0.91	0.365	-0.15	0.14	-1.06	0.290
South-West	Nmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	Nmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	Nmic	CWM_MycInt	Nmic	~	CWM_MycInt_historic	c	-0.02	0.11	-0.19	0.853	-0.03	0.14	-0.19	0.853
South-West	Nmic	CWM_MycInt	Nmic	~	CWM_MycInt_change	d	0.32	0.15	2.09	0.037	0.29	0.13	2.16	0.031
South-West	Nmic	CWM_MycInt	Nmic	~	LUI_historic	e	0.28	0.15	1.95	0.052	0.27	0.13	2.01	0.045
South-West	Nmic	CWM_MycInt	Nmic	~	LUI_change	f	-0.18	0.12	-1.46	0.145	-0.20	0.14	-1.48	0.139
South-West	Nmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	Nmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	Nmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	Nmic	CWM_MycInt	Nmic	~~	Nmic		0.03	0.01	4.90	0.000	0.83	0.10	8.65	0.000
South-West	Nmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Nmic	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Nmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.04	-0.18	0.854	-0.01	0.04	-0.18	0.854
South-West	Nmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.08	0.05	1.51	0.131	0.09	0.06	1.53	0.127
South-West	Nmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.28	0.14	1.97	0.048	0.26	0.13	2.04	0.042
South-West	Nmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.10	0.12	-0.83	0.404	-0.12	0.14	-0.84	0.401
South-West	Nmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.28	0.14	1.98	0.048	0.28	0.13	2.15	0.032
South-West	Nmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.12	-0.85	0.398	-0.15	0.14	-1.03	0.302
South-West	Nmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	Nmic	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	Nmic	Plant_biomass	Nmic	~	Plant_biomass	c	0.33	0.12	2.86	0.004	0.37	0.12	3.05	0.002
South-West	Nmic	Plant_biomass	Nmic	~	LUI_historic	e	0.19	0.14	1.39	0.164	0.18	0.13	1.41	0.159
South-West	Nmic	Plant_biomass	Nmic	~	LUI_change	f	-0.08	0.11	-0.78	0.439	-0.10	0.13	-0.78	0.437
South-West	Nmic	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	Nmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	Nmic	Plant_biomass	Nmic	~~	Nmic		0.03	0.01	5.00	0.000	0.79	0.10	7.76	0.000
South-West	Nmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Nmic	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Nmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.06	0.06	1.08	0.280	0.06	0.05	1.10	0.271
South-West	Nmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.04	-0.29	0.772	-0.02	0.05	-0.29	0.772
South-West	Nmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.25	0.14	1.75	0.081	0.24	0.13	1.80	0.073
South-West	Nmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.09	0.11	-0.83	0.408	-0.11	0.14	-0.83	0.405
South-West	Nmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.25	0.14	1.75	0.080	0.26	0.13	1.94	0.052
South-West	Nmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.11	-0.84	0.399	-0.15	0.14	-1.08	0.281

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
South-West	Nmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	Nmic	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	Nmic	Lignin_content	Nmic	~	Lignin_content	c	0.09	0.11	0.79	0.432	0.11	0.14	0.79	0.429
South-West	Nmic	Lignin_content	Nmic	~	LUI_historic	e	0.24	0.15	1.65	0.099	0.23	0.14	1.70	0.090
South-West	Nmic	Lignin_content	Nmic	~	LUI_change	f	-0.10	0.11	-0.83	0.406	-0.12	0.14	-0.84	0.403
South-West	Nmic	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	Nmic	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	Nmic	Lignin_content	Nmic	~~	Nmic		0.03	0.01	4.90	0.000	0.92	0.08	11.93	0.000
South-West	Nmic	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Nmic	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Nmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.13	0.897	0.00	0.02	0.13	0.897
South-West	Nmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.45	0.656	0.01	0.02	0.45	0.656
South-West	Nmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.24	0.15	1.66	0.098	0.23	0.14	1.70	0.089
South-West	Nmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.09	0.11	-0.77	0.443	-0.11	0.14	-0.77	0.440
South-West	Nmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.24	0.15	1.66	0.097	0.25	0.14	1.83	0.068
South-West	Nmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.11	-0.78	0.435	-0.14	0.14	-0.99	0.323
South-West	Nmic	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	Nmic	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	Nmic	pH	Nmic	~	pH_historic	c	-0.05	0.10	-0.48	0.633	-0.06	0.13	-0.48	0.633
South-West	Nmic	pH	Nmic	~	pH_change	d	0.26	0.13	2.02	0.044	0.26	0.13	2.08	0.038
South-West	Nmic	pH	Nmic	~	LUI_historic	e	0.28	0.14	1.99	0.046	0.26	0.13	2.05	0.040
South-West	Nmic	pH	Nmic	~	LUI_change	f	-0.11	0.11	-0.98	0.327	-0.13	0.13	-0.99	0.324
South-West	Nmic	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	Nmic	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	Nmic	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.94	0.000
South-West	Nmic	pH	Nmic	~~	Nmic		0.03	0.01	5.00	0.000	0.83	0.10	8.72	0.000
South-West	Nmic	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Nmic	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Nmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.39	0.698	0.01	0.02	0.39	0.698
South-West	Nmic	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.03	-0.08	0.933	0.00	0.04	-0.08	0.933
South-West	Nmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.28	0.14	2.04	0.041	0.27	0.13	2.11	0.035
South-West	Nmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.11	0.11	-0.97	0.334	-0.13	0.13	-0.97	0.330
South-West	Nmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.28	0.14	2.05	0.041	0.29	0.13	2.28	0.023
South-West	Nmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.11	0.11	-0.98	0.326	-0.17	0.14	-1.24	0.215
South-West	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	CWM_leafP_historic	c	0.07	0.18	0.40	0.691	0.08	0.20	0.40	0.690
South-West	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	CWM_leafP_change	d	-0.17	0.19	-0.93	0.353	-0.13	0.14	-0.94	0.349
South-West	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	LUI_historic	e	-0.34	0.25	-1.33	0.185	-0.27	0.20	-1.35	0.177
South-West	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	LUI_change	f	-0.01	0.15	-0.06	0.951	-0.01	0.14	-0.06	0.951
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	4.90	0.000	0.94	0.07	13.81	0.000
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.07	0.18	0.40	0.691	0.06	0.15	0.40	0.691
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.02	-0.48	0.628	-0.01	0.02	-0.49	0.627
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.26	0.18	-1.50	0.135	-0.21	0.14	-1.53	0.127
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.02	0.15	-0.14	0.892	-0.02	0.14	-0.14	0.892
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.26	0.18	-1.50	0.135	-0.21	0.14	-1.52	0.128
South-West	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.02	0.15	-0.13	0.899	0.01	0.14	0.04	0.972
South-West	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	CWM_MycInt_historic	c	0.10	0.14	0.74	0.460	0.11	0.14	0.74	0.458
South-West	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	CWM_MycInt_change	d	-0.17	0.19	-0.90	0.371	-0.13	0.14	-0.90	0.367
South-West	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	LUI_historic	e	-0.34	0.18	-1.86	0.063	-0.27	0.14	-1.92	0.055
South-West	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	LUI_change	f	0.02	0.15	0.16	0.875	0.02	0.15	0.16	0.875
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	4.90	0.000	0.92	0.08	12.15	0.000
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.04	0.06	0.70	0.486	0.03	0.04	0.70	0.485
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.04	0.05	-0.83	0.407	-0.04	0.05	-0.83	0.405
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.30	0.18	-1.71	0.088	-0.24	0.14	-1.76	0.079
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.02	0.15	-0.11	0.909	-0.02	0.14	-0.11	0.909
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.30	0.18	-1.71	0.088	-0.24	0.14	-1.76	0.079
South-West	Cmic:Nmic ratio	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.02	0.15	-0.10	0.917	0.01	0.14	0.08	0.936

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
South-West	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	Plant_biomass	c	-0.24	0.15	-1.62	0.106	-0.22	0.13	-1.65	0.098
South-West	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	LUI_historic	e	-0.22	0.18	-1.26	0.208	-0.17	0.14	-1.28	0.202
South-West	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	LUI_change	f	-0.07	0.14	-0.50	0.621	-0.07	0.14	-0.50	0.620
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	5.00	0.000	0.91	0.08	11.70	0.000
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.05	0.05	-0.95	0.345	-0.04	0.04	-0.96	0.338
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.03	0.29	0.775	0.01	0.03	0.29	0.775
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.27	0.18	-1.50	0.133	-0.21	0.14	-1.54	0.125
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.06	0.14	-0.42	0.676	-0.06	0.14	-0.42	0.676
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.27	0.18	-1.50	0.133	-0.20	0.14	-1.49	0.138
South-West	Cmic:Nmic ratio	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.06	0.14	-0.41	0.685	-0.03	0.14	-0.19	0.846
South-West	Cmic:Nmic ratio	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	Cmic:Nmic ratio	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	Lignin_content	c	-0.01	0.14	-0.08	0.935	-0.01	0.14	-0.08	0.935
South-West	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	LUI_historic	e	-0.24	0.18	-1.32	0.185	-0.19	0.14	-1.35	0.178
South-West	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	LUI_change	f	-0.07	0.14	-0.51	0.609	-0.07	0.14	-0.51	0.608
South-West	Cmic:Nmic ratio	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	Cmic:Nmic ratio	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	4.90	0.000	0.96	0.05	17.84	0.000
South-West	Cmic:Nmic ratio	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	-0.07	0.945	0.00	0.00	-0.07	0.945
South-West	Cmic:Nmic ratio	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	-0.08	0.936	0.00	0.01	-0.08	0.936
South-West	Cmic:Nmic ratio	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.24	0.18	-1.33	0.185	-0.19	0.14	-1.35	0.177
South-West	Cmic:Nmic ratio	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.07	0.14	-0.52	0.603	-0.07	0.14	-0.52	0.603
South-West	Cmic:Nmic ratio	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.24	0.18	-1.32	0.185	-0.18	0.14	-1.28	0.199
South-West	Cmic:Nmic ratio	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.07	0.14	-0.51	0.610	-0.05	0.14	-0.33	0.739
South-West	Cmic:Nmic ratio	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	Cmic:Nmic ratio	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	pH_historic	c	0.21	0.13	1.65	0.099	0.22	0.13	1.69	0.091
South-West	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	pH_change	d	-0.20	0.16	-1.24	0.216	-0.16	0.13	-1.25	0.211
South-West	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	LUI_historic	e	-0.25	0.17	-1.47	0.142	-0.20	0.13	-1.50	0.135
South-West	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	LUI_change	f	0.02	0.13	0.14	0.890	0.02	0.13	0.14	0.890
South-West	Cmic:Nmic ratio	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	Cmic:Nmic ratio	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	Cmic:Nmic ratio	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	5.00	0.000	0.88	0.09	10.15	0.000
South-West	Cmic:Nmic ratio	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	Cmic:Nmic ratio	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.03	0.04	-0.62	0.537	-0.02	0.03	-0.62	0.534
South-West	Cmic:Nmic ratio	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.02	0.08	0.933	0.00	0.02	0.08	0.933
South-West	Cmic:Nmic ratio	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.28	0.18	-1.59	0.112	-0.22	0.13	-1.63	0.104
South-West	Cmic:Nmic ratio	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.02	0.14	0.15	0.880	0.02	0.14	0.15	0.880
South-West	Cmic:Nmic ratio	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.28	0.18	-1.59	0.112	-0.22	0.13	-1.67	0.096
South-West	Cmic:Nmic ratio	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.14	0.16	0.870	0.05	0.14	0.38	0.702
South-West	Pmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.01	0.15	6.72	0.000	0.74	0.07	10.00	0.000
South-West	Pmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.12	0.12	1.02	0.308	0.17	0.16	1.03	0.301
South-West	Pmic	CWM_leaf_P	Pmic	~	CWM_leafP_historic	c	0.00	0.16	0.00	0.999	0.00	0.21	0.00	0.999
South-West	Pmic	CWM_leaf_P	Pmic	~	CWM_leafP_change	d	-0.08	0.17	-0.47	0.641	-0.07	0.15	-0.47	0.640
South-West	Pmic	CWM_leaf_P	Pmic	~	LUI_historic	e	0.49	0.21	2.29	0.022	0.49	0.20	2.42	0.015
South-West	Pmic	CWM_leaf_P	Pmic	~	LUI_change	f	0.07	0.12	0.56	0.575	0.08	0.15	0.56	0.575
South-West	Pmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	-0.38	0.701	-0.06	0.16	-0.39	0.699
South-West	Pmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.30	0.000	0.45	0.11	4.10	0.000
South-West	Pmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.30	0.000	0.97	0.05	18.40	0.000
South-West	Pmic	CWM_leaf_P	Pmic	~~	Pmic		0.03	0.01	4.30	0.000	0.76	0.12	6.18	0.000
South-West	Pmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.04	0.01	4.30	0.000	1.00	0.00	NA	NA
South-West	Pmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.06	0.01	4.30	0.000	1.00	0.00	NA	NA
South-West	Pmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.16	0.00	0.999	0.00	0.16	0.00	0.999
South-West	Pmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.02	-0.42	0.671	-0.01	0.03	-0.43	0.671
South-West	Pmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.49	0.14	3.41	0.001	0.49	0.13	3.89	0.000
South-West	Pmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.06	0.12	0.49	0.625	0.07	0.14	0.49	0.625
South-West	Pmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.49	0.14	3.41	0.001	0.48	0.13	3.85	0.000
South-West	Pmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.06	0.12	0.48	0.634	0.04	0.16	0.24	0.810

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
South-West	Pmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.28	0.19	1.50	0.134	0.24	0.16	1.55	0.122
South-West	Pmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.18	0.11	1.67	0.095	0.27	0.15	1.73	0.083
South-West	Pmic	CWM_MycInt	Pmic	~	CWM_MycInt_historic	c	0.01	0.12	0.06	0.950	0.01	0.15	0.06	0.950
South-West	Pmic	CWM_MycInt	Pmic	~	CWM_MycInt_change	d	0.22	0.18	1.22	0.224	0.18	0.15	1.23	0.219
South-West	Pmic	CWM_MycInt	Pmic	~	LUI_historic	e	0.46	0.15	3.17	0.002	0.47	0.13	3.53	0.000
South-West	Pmic	CWM_MycInt	Pmic	~	LUI_change	f	0.02	0.12	0.15	0.885	0.02	0.15	0.15	0.885
South-West	Pmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	-0.38	0.701	-0.06	0.16	-0.39	0.699
South-West	Pmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.30	0.000	0.94	0.07	12.70	0.000
South-West	Pmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.02	0.01	4.30	0.000	0.93	0.08	11.48	0.000
South-West	Pmic	CWM_MycInt	Pmic	~~	Pmic		0.03	0.01	4.30	0.000	0.75	0.12	6.17	0.000
South-West	Pmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.04	0.01	4.30	0.000	1.00	0.00	NA	NA
South-West	Pmic	CWM_MycInt	LUI_change	~~	LUI_change		0.06	0.01	4.30	0.000	1.00	0.00	NA	NA
South-West	Pmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.04	0.06	0.950	0.00	0.04	0.06	0.950
South-West	Pmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.04	0.04	0.98	0.325	0.05	0.05	0.99	0.322
South-West	Pmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.46	0.14	3.28	0.001	0.47	0.13	3.69	0.000
South-West	Pmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.06	0.12	0.47	0.635	0.07	0.15	0.48	0.635
South-West	Pmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.46	0.14	3.28	0.001	0.46	0.13	3.64	0.000
South-West	Pmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.06	0.12	0.46	0.643	0.04	0.16	0.24	0.810
South-West	Pmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.29	0.17	1.69	0.091	0.26	0.15	1.75	0.080
South-West	Pmic	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.03	0.14	-0.19	0.852	-0.03	0.16	-0.19	0.852
South-West	Pmic	Plant_biomass	Pmic	~	Plant_biomass	c	0.21	0.15	1.44	0.151	0.21	0.14	1.46	0.145
South-West	Pmic	Plant_biomass	Pmic	~	LUI_historic	e	0.47	0.17	2.85	0.004	0.41	0.13	3.08	0.002
South-West	Pmic	Plant_biomass	Pmic	~	LUI_change	f	-0.06	0.13	-0.46	0.645	-0.06	0.14	-0.46	0.645
South-West	Pmic	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.68	0.499	-0.11	0.16	-0.69	0.492
South-West	Pmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	4.42	0.000	0.93	0.08	11.70	0.000
South-West	Pmic	Plant_biomass	Pmic	~~	Pmic		0.04	0.01	4.42	0.000	0.74	0.12	6.08	0.000
South-West	Pmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.04	0.01	4.42	0.000	1.00	0.00	NA	NA
South-West	Pmic	Plant_biomass	LUI_change	~~	LUI_change		0.06	0.01	4.42	0.000	1.00	0.00	NA	NA
South-West	Pmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.06	0.06	1.09	0.274	0.05	0.05	1.12	0.264
South-West	Pmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.03	-0.19	0.853	-0.01	0.03	-0.19	0.853
South-West	Pmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.54	0.17	3.26	0.001	0.46	0.13	3.66	0.000
South-West	Pmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.06	0.13	-0.49	0.623	-0.07	0.14	-0.49	0.623
South-West	Pmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.54	0.17	3.26	0.001	0.47	0.13	3.76	0.000
South-West	Pmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.07	0.13	-0.51	0.609	-0.12	0.16	-0.76	0.447
South-West	Pmic	Lignin_content	Lignin_content	~	LUI_historic	a	-0.08	0.20	-0.38	0.701	-0.06	0.16	-0.39	0.700
South-West	Pmic	Lignin_content	Lignin_content	~	LUI_change	b	0.17	0.16	1.09	0.277	0.18	0.16	1.10	0.270
South-West	Pmic	Lignin_content	Pmic	~	Lignin_content	c	0.04	0.14	0.31	0.757	0.05	0.15	0.31	0.757
South-West	Pmic	Lignin_content	Pmic	~	LUI_historic	e	0.50	0.17	3.04	0.002	0.45	0.13	3.39	0.001
South-West	Pmic	Lignin_content	Pmic	~	LUI_change	f	-0.06	0.13	-0.45	0.653	-0.07	0.15	-0.45	0.653
South-West	Pmic	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.59	0.553	-0.10	0.16	-0.60	0.548
South-West	Pmic	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.30	0.000	0.96	0.06	15.79	0.000
South-West	Pmic	Lignin_content	Pmic	~~	Pmic		0.04	0.01	4.30	0.000	0.79	0.12	6.66	0.000
South-West	Pmic	Lignin_content	LUI_historic	~~	LUI_historic		0.04	0.01	4.30	0.000	1.00	0.00	NA	NA
South-West	Pmic	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.30	0.000	1.00	0.00	NA	NA
South-West	Pmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.24	0.810	0.00	0.01	-0.24	0.810
South-West	Pmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.30	0.766	0.01	0.03	0.30	0.766
South-West	Pmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.50	0.17	3.02	0.003	0.45	0.13	3.37	0.001
South-West	Pmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.05	0.13	-0.40	0.689	-0.06	0.15	-0.40	0.688
South-West	Pmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.50	0.17	3.02	0.003	0.45	0.13	3.44	0.001
South-West	Pmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.06	0.13	-0.42	0.675	-0.10	0.16	-0.63	0.529
South-West	Pmic	pH	pH_historic	~	LUI_historic	a	-0.26	0.21	-1.25	0.213	-0.20	0.15	-1.27	0.204
South-West	Pmic	pH	pH_change	~	LUI_change	b	0.08	0.11	0.70	0.484	0.11	0.16	0.70	0.481
South-West	Pmic	pH	Pmic	~	pH_historic	c	-0.11	0.13	-0.90	0.370	-0.13	0.14	-0.90	0.367
South-West	Pmic	pH	Pmic	~	pH_change	d	-0.02	0.19	-0.08	0.939	-0.01	0.14	-0.08	0.939
South-West	Pmic	pH	Pmic	~	LUI_historic	e	0.50	0.17	2.99	0.003	0.43	0.13	3.28	0.001
South-West	Pmic	pH	Pmic	~	LUI_change	f	-0.11	0.13	-0.85	0.394	-0.12	0.14	-0.86	0.392
South-West	Pmic	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.68	0.499	-0.11	0.16	-0.69	0.492
South-West	Pmic	pH	pH_historic	~~	pH_historic		0.06	0.01	4.42	0.000	0.96	0.06	15.97	0.000
South-West	Pmic	pH	pH_change	~~	pH_change		0.03	0.01	4.42	0.000	0.99	0.04	28.04	0.000
South-West	Pmic	pH	Pmic	~~	Pmic		0.04	0.01	4.42	0.000	0.75	0.12	6.30	0.000
South-West	Pmic	pH	LUI_historic	~~	LUI_historic		0.04	0.01	4.42	0.000	1.00	0.00	NA	NA
South-West	Pmic	pH	LUI_change	~~	LUI_change		0.06	0.01	4.42	0.000	1.00	0.00	NA	NA
South-West	Pmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.04	0.73	0.467	0.03	0.03	0.74	0.463
South-West	Pmic	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.02	-0.08	0.939	0.00	0.02	-0.08	0.939
South-West	Pmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.53	0.17	3.19	0.001	0.45	0.13	3.57	0.000
South-West	Pmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.11	0.13	-0.87	0.387	-0.12	0.14	-0.87	0.384
South-West	Pmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.53	0.17	3.20	0.001	0.47	0.13	3.70	0.000
South-West	Pmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.12	0.13	-0.89	0.375	-0.17	0.15	-1.10	0.270

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
South-West	beta-glucosidase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	beta-glucosidase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	beta-glucosidase	CWM_leaf_P	Glucosidase	~	CWM_leafP_historic	c	0.42	0.15	2.71	0.007	0.48	0.17	2.84	0.005
South-West	beta-glucosidase	CWM_leaf_P	Glucosidase	~	CWM_leafP_change	d	0.33	0.16	2.04	0.042	0.25	0.12	2.08	0.038
South-West	beta-glucosidase	CWM_leaf_P	Glucosidase	~	LUI_historic	e	-0.16	0.22	-0.73	0.466	-0.13	0.18	-0.73	0.465
South-West	beta-glucosidase	CWM_leaf_P	Glucosidase	~	LUI_change	f	-0.28	0.13	-2.24	0.025	-0.27	0.12	-2.30	0.021
South-West	beta-glucosidase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	beta-glucosidase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	beta-glucosidase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	beta-glucosidase	CWM_leaf_P	Glucosidase	~~	Glucosidase		0.04	0.01	4.90	0.000	0.71	0.11	6.59	0.000
South-West	beta-glucosidase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.43	0.17	2.54	0.011	0.34	0.13	2.65	0.008
South-West	beta-glucosidase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.55	0.585	0.02	0.04	0.55	0.586
South-West	beta-glucosidase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.27	0.17	1.64	0.102	0.22	0.13	1.67	0.095
South-West	beta-glucosidase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.26	0.13	-2.00	0.046	-0.25	0.12	-2.05	0.040
South-West	beta-glucosidase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.27	0.17	1.65	0.100	0.24	0.13	1.86	0.063
South-West	beta-glucosidase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.27	0.13	-2.01	0.045	-0.28	0.13	-2.22	0.026
South-West	beta-glucosidase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	beta-glucosidase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	beta-glucosidase	CWM_MycInt	Glucosidase	~	CWM_MycInt_historic	c	0.11	0.13	0.79	0.427	0.11	0.14	0.80	0.425
South-West	beta-glucosidase	CWM_MycInt	Glucosidase	~	CWM_MycInt_change	d	-0.07	0.18	-0.38	0.706	-0.05	0.14	-0.38	0.706
South-West	beta-glucosidase	CWM_MycInt	Glucosidase	~	LUI_historic	e	0.29	0.18	1.67	0.095	0.24	0.14	1.71	0.087
South-West	beta-glucosidase	CWM_MycInt	Glucosidase	~	LUI_change	f	-0.16	0.14	-1.08	0.279	-0.15	0.14	-1.09	0.274
South-West	beta-glucosidase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	beta-glucosidase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	beta-glucosidase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	beta-glucosidase	CWM_MycInt	Glucosidase	~~	Glucosidase		0.05	0.01	4.90	0.000	0.87	0.09	9.78	0.000
South-West	beta-glucosidase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.04	0.05	0.74	0.458	0.03	0.04	0.75	0.455
South-West	beta-glucosidase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.04	-0.37	0.710	-0.02	0.04	-0.37	0.710
South-West	beta-glucosidase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.33	0.17	1.97	0.049	0.27	0.13	2.04	0.041
South-West	beta-glucosidase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.17	0.14	-1.25	0.211	-0.17	0.13	-1.27	0.205
South-West	beta-glucosidase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.33	0.17	1.97	0.048	0.29	0.13	2.19	0.029
South-West	beta-glucosidase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.17	0.14	-1.26	0.207	-0.20	0.14	-1.46	0.144
South-West	beta-glucosidase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	beta-glucosidase	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	beta-glucosidase	Plant_biomass	Glucosidase	~	Plant_biomass	c	0.25	0.14	1.73	0.083	0.23	0.13	1.77	0.077
South-West	beta-glucosidase	Plant_biomass	Glucosidase	~	LUI_historic	e	0.30	0.17	1.83	0.068	0.24	0.13	1.87	0.061
South-West	beta-glucosidase	Plant_biomass	Glucosidase	~	LUI_change	f	-0.17	0.13	-1.30	0.192	-0.17	0.13	-1.32	0.187
South-West	beta-glucosidase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	beta-glucosidase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	beta-glucosidase	Plant_biomass	Glucosidase	~~	Glucosidase		0.04	0.01	5.00	0.000	0.83	0.10	8.49	0.000
South-West	beta-glucosidase	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.05	0.05	0.97	0.334	0.04	0.04	0.98	0.327
South-West	beta-glucosidase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.03	-0.29	0.774	-0.01	0.03	-0.29	0.774
South-West	beta-glucosidase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.35	0.17	2.07	0.038	0.28	0.13	2.15	0.031
South-West	beta-glucosidase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.18	0.13	-1.34	0.181	-0.18	0.13	-1.36	0.175
South-West	beta-glucosidase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.35	0.17	2.08	0.037	0.30	0.13	2.37	0.018
South-West	beta-glucosidase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.18	0.13	-1.36	0.175	-0.22	0.14	-1.63	0.102
South-West	beta-glucosidase	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	beta-glucosidase	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	beta-glucosidase	Lignin_content	Glucosidase	~	Lignin_content	c	-0.04	0.13	-0.34	0.734	-0.05	0.14	-0.34	0.734
South-West	beta-glucosidase	Lignin_content	Glucosidase	~	LUI_historic	e	0.34	0.17	2.03	0.043	0.28	0.13	2.10	0.035
South-West	beta-glucosidase	Lignin_content	Glucosidase	~	LUI_change	f	-0.16	0.13	-1.24	0.216	-0.17	0.14	-1.25	0.210
South-West	beta-glucosidase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	beta-glucosidase	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	beta-glucosidase	Lignin_content	Glucosidase	~~	Glucosidase		0.05	0.01	4.90	0.000	0.88	0.09	9.94	0.000
South-West	beta-glucosidase	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.12	0.902	0.00	0.01	-0.12	0.903
South-West	beta-glucosidase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	-0.29	0.774	0.00	0.01	-0.29	0.774
South-West	beta-glucosidase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.34	0.17	2.02	0.044	0.28	0.13	2.10	0.036
South-West	beta-glucosidase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.17	0.13	-1.27	0.206	-0.17	0.14	-1.28	0.200
South-West	beta-glucosidase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.34	0.17	2.03	0.043	0.30	0.13	2.28	0.022
South-West	beta-glucosidase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.17	0.13	-1.28	0.200	-0.21	0.14	-1.53	0.126

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
South-West	beta-glucosidase	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	beta-glucosidase	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	beta-glucosidase	pH	Glucosidase	~	pH_historic	c	-0.27	0.12	-2.25	0.025	-0.27	0.12	-2.31	0.021
South-West	beta-glucosidase	pH	Glucosidase	~	pH_change	d	0.20	0.15	1.33	0.183	0.16	0.12	1.34	0.179
South-West	beta-glucosidase	pH	Glucosidase	~	LUI_historic	e	0.32	0.16	2.03	0.042	0.25	0.12	2.08	0.037
South-West	beta-glucosidase	pH	Glucosidase	~	LUI_change	f	-0.28	0.13	-2.22	0.027	-0.27	0.12	-2.28	0.023
South-West	beta-glucosidase	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	beta-glucosidase	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	beta-glucosidase	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	beta-glucosidase	pH	Glucosidase	~~	Glucosidase		0.04	0.01	5.00	0.000	0.73	0.11	6.91	0.000
South-West	beta-glucosidase	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-glucosidase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.05	0.64	0.523	0.03	0.04	0.65	0.519
South-West	beta-glucosidase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.02	-0.08	0.933	0.00	0.02	-0.08	0.933
South-West	beta-glucosidase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.36	0.17	2.15	0.032	0.28	0.12	2.23	0.026
South-West	beta-glucosidase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.28	0.13	-2.19	0.028	-0.27	0.12	-2.26	0.024
South-West	beta-glucosidase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.36	0.17	2.16	0.031	0.32	0.13	2.51	0.012
South-West	beta-glucosidase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.28	0.13	-2.21	0.027	-0.31	0.12	-2.55	0.011
South-West	beta-xylosidase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	beta-xylosidase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	beta-xylosidase	CWM_leaf_P	Xylosidase	~	CWM_leafP_historic	c	0.42	0.15	2.87	0.004	0.51	0.17	3.04	0.002
South-West	beta-xylosidase	CWM_leaf_P	Xylosidase	~	CWM_leafP_change	d	0.13	0.16	0.85	0.398	0.10	0.12	0.85	0.396
South-West	beta-xylosidase	CWM_leaf_P	Xylosidase	~	LUI_historic	e	-0.17	0.21	-0.77	0.439	-0.14	0.18	-0.78	0.437
South-West	beta-xylosidase	CWM_leaf_P	Xylosidase	~	LUI_change	f	-0.29	0.12	-2.37	0.018	-0.29	0.12	-2.45	0.014
South-West	beta-xylosidase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	beta-xylosidase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	beta-xylosidase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	beta-xylosidase	CWM_leaf_P	Xylosidase	~~	Xylosidase		0.04	0.01	4.90	0.000	0.72	0.11	6.66	0.000
South-West	beta-xylosidase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.44	0.17	2.67	0.008	0.37	0.13	2.82	0.005
South-West	beta-xylosidase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.02	0.47	0.637	0.01	0.02	0.47	0.638
South-West	beta-xylosidase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.28	0.16	1.72	0.086	0.23	0.13	1.76	0.078
South-West	beta-xylosidase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.28	0.12	-2.29	0.022	-0.28	0.12	-2.37	0.018
South-West	beta-xylosidase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.28	0.16	1.73	0.084	0.26	0.13	1.96	0.050
South-West	beta-xylosidase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.28	0.12	-2.31	0.021	-0.31	0.12	-2.55	0.011
South-West	beta-xylosidase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	beta-xylosidase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	beta-xylosidase	CWM_MycInt	Xylosidase	~	CWM_MycInt_historic	c	0.05	0.13	0.42	0.672	0.06	0.14	0.42	0.672
South-West	beta-xylosidase	CWM_MycInt	Xylosidase	~	CWM_MycInt_change	d	-0.07	0.17	-0.41	0.683	-0.06	0.14	-0.41	0.682
South-West	beta-xylosidase	CWM_MycInt	Xylosidase	~	LUI_historic	e	0.28	0.17	1.72	0.085	0.24	0.14	1.77	0.077
South-West	beta-xylosidase	CWM_MycInt	Xylosidase	~	LUI_change	f	-0.17	0.14	-1.24	0.216	-0.18	0.14	-1.25	0.210
South-West	beta-xylosidase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	beta-xylosidase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	beta-xylosidase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	beta-xylosidase	CWM_MycInt	Xylosidase	~~	Xylosidase		0.04	0.01	4.90	0.000	0.88	0.09	9.86	0.000
South-West	beta-xylosidase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.05	0.41	0.679	0.02	0.04	0.42	0.678
South-West	beta-xylosidase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.04	-0.40	0.688	-0.02	0.04	-0.40	0.687
South-West	beta-xylosidase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.30	0.16	1.92	0.055	0.26	0.13	1.98	0.047
South-West	beta-xylosidase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.19	0.13	-1.42	0.155	-0.19	0.13	-1.45	0.148
South-West	beta-xylosidase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.31	0.16	1.92	0.054	0.28	0.13	2.14	0.032
South-West	beta-xylosidase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.19	0.13	-1.43	0.152	-0.22	0.14	-1.64	0.102
South-West	beta-xylosidase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	beta-xylosidase	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	beta-xylosidase	Plant_biomass	Xylosidase	~	Plant_biomass	c	-0.03	0.14	-0.23	0.818	-0.03	0.14	-0.23	0.818
South-West	beta-xylosidase	Plant_biomass	Xylosidase	~	LUI_historic	e	0.31	0.16	1.96	0.050	0.27	0.13	2.02	0.043
South-West	beta-xylosidase	Plant_biomass	Xylosidase	~	LUI_change	f	-0.16	0.12	-1.33	0.183	-0.18	0.13	-1.35	0.176
South-West	beta-xylosidase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	beta-xylosidase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	beta-xylosidase	Plant_biomass	Xylosidase	~~	Xylosidase		0.04	0.01	5.00	0.000	0.89	0.09	10.43	0.000
South-West	beta-xylosidase	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.23	0.821	-0.01	0.02	-0.23	0.821
South-West	beta-xylosidase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.18	0.857	0.00	0.01	0.18	0.857
South-West	beta-xylosidase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.30	0.16	1.94	0.052	0.26	0.13	2.01	0.044
South-West	beta-xylosidase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.16	0.12	-1.32	0.186	-0.18	0.13	-1.34	0.179
South-West	beta-xylosidase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.30	0.16	1.95	0.051	0.29	0.13	2.22	0.026
South-West	beta-xylosidase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.16	0.12	-1.34	0.180	-0.22	0.14	-1.61	0.108

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
South-West	beta-xylosidase	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	beta-xylosidase	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	beta-xylosidase	Lignin_content	Xylosidase	~	Lignin_content	c	0.00	0.12	0.02	0.984	0.00	0.14	0.02	0.984
South-West	beta-xylosidase	Lignin_content	Xylosidase	~	LUI_historic	e	0.30	0.16	1.92	0.055	0.26	0.13	1.99	0.047
South-West	beta-xylosidase	Lignin_content	Xylosidase	~	LUI_change	f	-0.16	0.12	-1.27	0.205	-0.18	0.14	-1.29	0.199
South-West	beta-xylosidase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	beta-xylosidase	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	beta-xylosidase	Lignin_content	Xylosidase	~~	Xylosidase		0.04	0.01	4.90	0.000	0.89	0.09	10.31	0.000
South-West	beta-xylosidase	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	0.02	0.984	0.00	0.00	0.02	0.984
South-West	beta-xylosidase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.02	0.984	0.00	0.01	0.02	0.984
South-West	beta-xylosidase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.30	0.16	1.92	0.054	0.26	0.13	1.99	0.047
South-West	beta-xylosidase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.16	0.12	-1.27	0.204	-0.17	0.14	-1.29	0.198
South-West	beta-xylosidase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.31	0.16	1.93	0.054	0.29	0.13	2.18	0.030
South-West	beta-xylosidase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.16	0.12	-1.29	0.198	-0.21	0.14	-1.53	0.126
South-West	beta-xylosidase	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	beta-xylosidase	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	beta-xylosidase	pH	Xylosidase	~	pH_historic	c	-0.20	0.11	-1.89	0.058	-0.22	0.12	-1.92	0.054
South-West	beta-xylosidase	pH	Xylosidase	~	pH_change	d	0.37	0.13	2.80	0.005	0.33	0.11	2.91	0.004
South-West	beta-xylosidase	pH	Xylosidase	~	LUI_historic	e	0.31	0.14	2.22	0.026	0.26	0.12	2.28	0.023
South-West	beta-xylosidase	pH	Xylosidase	~	LUI_change	f	-0.23	0.11	-2.09	0.037	-0.25	0.12	-2.13	0.033
South-West	beta-xylosidase	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	beta-xylosidase	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	beta-xylosidase	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	beta-xylosidase	pH	Xylosidase	~~	Xylosidase		0.03	0.01	5.00	0.000	0.68	0.11	6.42	0.000
South-West	beta-xylosidase	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	beta-xylosidase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.04	0.63	0.530	0.02	0.03	0.63	0.527
South-West	beta-xylosidase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.04	-0.08	0.933	0.00	0.05	-0.08	0.933
South-West	beta-xylosidase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.34	0.15	2.33	0.020	0.28	0.12	2.40	0.016
South-West	beta-xylosidase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.23	0.12	-1.98	0.048	-0.25	0.12	-2.03	0.042
South-West	beta-xylosidase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.34	0.15	2.34	0.019	0.32	0.12	2.68	0.007
South-West	beta-xylosidase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.24	0.12	-2.00	0.046	-0.29	0.13	-2.32	0.021
South-West	chitinase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.15	7.09	0.000	0.73	0.07	10.31	0.000
South-West	chitinase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.10	-0.51	0.607	-0.08	0.15	-0.52	0.606
South-West	chitinase	CWM_leaf_P	Chitinase	~	CWM_leafP_historic	c	0.04	0.15	0.27	0.789	0.06	0.21	0.27	0.789
South-West	chitinase	CWM_leaf_P	Chitinase	~	CWM_leafP_change	d	0.01	0.19	0.06	0.952	0.01	0.15	0.06	0.952
South-West	chitinase	CWM_leaf_P	Chitinase	~	LUI_historic	e	-0.05	0.22	-0.24	0.808	-0.05	0.22	-0.24	0.808
South-West	chitinase	CWM_leaf_P	Chitinase	~	LUI_change	f	-0.14	0.13	-1.11	0.268	-0.17	0.15	-1.12	0.262
South-West	chitinase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.07	0.285	-0.16	0.15	-1.11	0.267
South-West	chitinase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.04	0.01	4.74	0.000	0.47	0.10	4.62	0.000
South-West	chitinase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.01	4.74	0.000	0.99	0.02	43.86	0.000
South-West	chitinase	CWM_leaf_P	Chitinase	~~	Chitinase		0.04	0.01	4.74	0.000	0.97	0.05	19.80	0.000
South-West	chitinase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
South-West	chitinase	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.74	0.000	1.00	0.00	NA	NA
South-West	chitinase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.04	0.16	0.27	0.789	0.04	0.16	0.27	0.789
South-West	chitinase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.06	0.952	0.00	0.01	-0.06	0.952
South-West	chitinase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.01	0.15	-0.07	0.943	-0.01	0.15	-0.07	0.943
South-West	chitinase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.14	0.13	-1.12	0.265	-0.17	0.15	-1.13	0.258
South-West	chitinase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.01	0.15	-0.07	0.948	0.02	0.15	0.11	0.914
South-West	chitinase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.14	0.13	-1.12	0.264	-0.16	0.15	-1.13	0.257
South-West	chitinase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.40	0.19	2.14	0.032	0.30	0.14	2.25	0.025
South-West	chitinase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.18	0.11	1.67	0.095	0.24	0.14	1.72	0.086
South-West	chitinase	CWM_MycInt	Chitinase	~	CWM_MycInt_historic	c	-0.10	0.12	-0.84	0.403	-0.13	0.15	-0.84	0.400
South-West	chitinase	CWM_MycInt	Chitinase	~	CWM_MycInt_change	d	-0.11	0.17	-0.63	0.529	-0.10	0.15	-0.63	0.527
South-West	chitinase	CWM_MycInt	Chitinase	~	LUI_historic	e	0.02	0.16	0.13	0.897	0.02	0.16	0.13	0.897
South-West	chitinase	CWM_MycInt	Chitinase	~	LUI_change	f	-0.10	0.13	-0.76	0.447	-0.12	0.15	-0.77	0.445
South-West	chitinase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.07	0.285	-0.16	0.15	-1.11	0.267
South-West	chitinase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.06	0.01	4.74	0.000	0.91	0.08	11.04	0.000
South-West	chitinase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.74	0.000	0.94	0.07	13.90	0.000
South-West	chitinase	CWM_MycInt	Chitinase	~~	Chitinase		0.04	0.01	4.74	0.000	0.96	0.06	16.44	0.000
South-West	chitinase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
South-West	chitinase	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.74	0.000	1.00	0.00	NA	NA
South-West	chitinase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.04	0.05	-0.78	0.436	-0.04	0.05	-0.78	0.433
South-West	chitinase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.03	-0.59	0.556	-0.02	0.04	-0.59	0.554
South-West	chitinase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.02	0.15	-0.13	0.899	-0.02	0.15	-0.13	0.899
South-West	chitinase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.12	0.13	-0.93	0.351	-0.14	0.15	-0.94	0.346
South-West	chitinase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.02	0.15	-0.12	0.903	0.00	0.15	0.02	0.982
South-West	chitinase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.12	0.13	-0.93	0.351	-0.14	0.15	-0.93	0.351

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P*.std
South-West	chitinase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.18	0.17	1.08	0.279	0.16	0.15	1.10	0.273
South-West	chitinase	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.03	0.13	-0.24	0.809	-0.04	0.15	-0.24	0.809
South-West	chitinase	Plant_biomass	Chitinase	~	Plant_biomass	c	0.11	0.13	0.84	0.399	0.12	0.14	0.85	0.396
South-West	chitinase	Plant_biomass	Chitinase	~	LUI_historic	e	-0.03	0.15	-0.19	0.853	-0.03	0.15	-0.19	0.853
South-West	chitinase	Plant_biomass	Chitinase	~	LUI_change	f	-0.12	0.12	-0.97	0.332	-0.14	0.15	-0.98	0.327
South-West	chitinase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.29	0.198	-0.19	0.14	-1.36	0.174
South-West	chitinase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	4.85	0.000	0.97	0.05	20.30	0.000
South-West	chitinase	Plant_biomass	Chitinase	~~	Chitinase		0.03	0.01	4.85	0.000	0.96	0.05	18.18	0.000
South-West	chitinase	Plant_biomass	LUI_historic	~~	LUI_historic		0.04	0.01	4.85	0.000	1.00	0.00	NA	NA
South-West	chitinase	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	4.85	0.000	1.00	0.00	NA	NA
South-West	chitinase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.03	0.67	0.506	0.02	0.03	0.67	0.504
South-West	chitinase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.02	-0.23	0.816	0.00	0.02	-0.23	0.816
South-West	chitinase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.01	0.15	-0.05	0.957	-0.01	0.15	-0.05	0.957
South-West	chitinase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.12	0.12	-0.99	0.321	-0.15	0.15	-1.00	0.316
South-West	chitinase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.01	0.15	-0.05	0.962	0.02	0.15	0.14	0.891
South-West	chitinase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.12	0.12	-1.00	0.320	-0.15	0.14	-1.01	0.312
South-West	chitinase	Lignin_content	Lignin_content	~	LUI_historic	a	-0.03	0.20	-0.16	0.876	-0.02	0.15	-0.16	0.876
South-West	chitinase	Lignin_content	Lignin_content	~	LUI_change	b	0.03	0.16	0.19	0.854	0.03	0.15	0.19	0.853
South-West	chitinase	Lignin_content	Chitinase	~	Lignin_content	c	-0.08	0.11	-0.74	0.459	-0.11	0.15	-0.75	0.456
South-West	chitinase	Lignin_content	Chitinase	~	LUI_historic	e	0.02	0.15	0.11	0.909	0.02	0.15	0.11	0.909
South-West	chitinase	Lignin_content	Chitinase	~	LUI_change	f	-0.12	0.12	-1.00	0.320	-0.15	0.15	-1.01	0.315
South-West	chitinase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.21	0.228	-0.18	0.14	-1.27	0.205
South-West	chitinase	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.74	0.000	1.00	0.01	84.30	0.000
South-West	chitinase	Lignin_content	Chitinase	~~	Chitinase		0.03	0.01	4.74	0.000	0.96	0.06	17.66	0.000
South-West	chitinase	Lignin_content	LUI_historic	~~	LUI_historic		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
South-West	chitinase	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.74	0.000	1.00	0.00	NA	NA
South-West	chitinase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.15	0.879	0.00	0.02	0.15	0.879
South-West	chitinase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	-0.18	0.858	0.00	0.02	-0.18	0.858
South-West	chitinase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.02	0.15	0.13	0.896	0.02	0.15	0.13	0.896
South-West	chitinase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.12	0.12	-1.01	0.313	-0.15	0.15	-1.02	0.307
South-West	chitinase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.02	0.15	0.14	0.891	0.05	0.15	0.32	0.751
South-West	chitinase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.12	0.12	-1.01	0.311	-0.16	0.15	-1.06	0.288
South-West	chitinase	pH	pH_historic	~	LUI_historic	a	-0.08	0.19	-0.44	0.661	-0.06	0.15	-0.44	0.660
South-West	chitinase	pH	pH_change	~	LUI_change	b	-0.02	0.13	-0.15	0.884	-0.02	0.15	-0.15	0.884
South-West	chitinase	pH	Chitinase	~	pH_historic	c	-0.26	0.10	-2.46	0.014	-0.33	0.13	-2.58	0.010
South-West	chitinase	pH	Chitinase	~	pH_change	d	0.09	0.13	0.72	0.473	0.10	0.13	0.72	0.472
South-West	chitinase	pH	Chitinase	~	LUI_historic	e	-0.04	0.14	-0.29	0.775	-0.04	0.14	-0.29	0.775
South-West	chitinase	pH	Chitinase	~	LUI_change	f	-0.21	0.11	-1.89	0.059	-0.25	0.13	-1.94	0.052
South-West	chitinase	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.29	0.198	-0.19	0.14	-1.36	0.174
South-West	chitinase	pH	pH_historic	~~	pH_historic		0.06	0.01	4.85	0.000	1.00	0.02	53.70	0.000
South-West	chitinase	pH	pH_change	~~	pH_change		0.04	0.01	4.85	0.000	1.00	0.01	160.82	0.000
South-West	chitinase	pH	Chitinase	~~	Chitinase		0.03	0.01	4.85	0.000	0.82	0.10	8.29	0.000
South-West	chitinase	pH	LUI_historic	~~	LUI_historic		0.04	0.01	4.85	0.000	1.00	0.00	NA	NA
South-West	chitinase	pH	LUI_change	~~	LUI_change		0.05	0.01	4.85	0.000	1.00	0.00	NA	NA
South-West	chitinase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.05	0.43	0.666	0.02	0.05	0.43	0.665
South-West	chitinase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.14	0.886	0.00	0.01	-0.14	0.886
South-West	chitinase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.02	0.15	-0.13	0.901	-0.02	0.14	-0.13	0.901
South-West	chitinase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.21	0.11	-1.89	0.058	-0.26	0.13	-1.95	0.051
South-West	chitinase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.02	0.15	-0.11	0.910	0.03	0.15	0.22	0.830
South-West	chitinase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.21	0.11	-1.90	0.058	-0.25	0.13	-1.96	0.051
South-West	urease	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	urease	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	urease	CWM_leaf_P	Urease	~	CWM_leafP_historic	c	-0.30	0.14	-2.13	0.033	-0.40	0.18	-2.22	0.027
South-West	urease	CWM_leaf_P	Urease	~	CWM_leafP_change	d	0.26	0.15	1.79	0.074	0.24	0.13	1.83	0.067
South-West	urease	CWM_leaf_P	Urease	~	LUI_historic	e	0.10	0.20	0.47	0.637	0.09	0.19	0.47	0.637
South-West	urease	CWM_leaf_P	Urease	~	LUI_change	f	0.02	0.12	0.15	0.880	0.02	0.13	0.15	0.880
South-West	urease	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	urease	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	urease	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	urease	CWM_leaf_P	Urease	~~	Urease		0.03	0.01	4.90	0.000	0.82	0.10	8.40	0.000
South-West	urease	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	urease	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	urease	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.31	0.15	-2.05	0.041	-0.29	0.14	-2.12	0.034
South-West	urease	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.03	0.54	0.589	0.02	0.04	0.54	0.587
South-West	urease	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.21	0.15	-1.46	0.143	-0.20	0.14	-1.49	0.136
South-West	urease	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.03	0.12	0.29	0.773	0.04	0.14	0.29	0.773
South-West	urease	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.21	0.15	-1.47	0.143	-0.21	0.13	-1.54	0.125
South-West	urease	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.04	0.12	0.30	0.766	0.06	0.14	0.45	0.651

Table S6.2 continued

Region	**MO variable**	**mediator**	**lhs**	**op**	**rhs**	**label**	**est**	**se**	**z**	***P***	**est.std**	**se.std**	**z.std**	***P*.std**
South-West	urease	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	urease	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	urease	CWM_MycInt	Urease	~	CWM_MycInt_historic	c	-0.31	0.11	-2.82	0.005	-0.39	0.13	-3.03	0.002
South-West	urease	CWM_MycInt	Urease	~	CWM_MycInt_change	d	0.05	0.15	0.30	0.765	0.04	0.14	0.30	0.765
South-West	urease	CWM_MycInt	Urease	~	LUI_historic	e	-0.06	0.15	-0.40	0.688	-0.06	0.14	-0.40	0.688
South-West	urease	CWM_MycInt	Urease	~	LUI_change	f	-0.01	0.12	-0.11	0.915	-0.02	0.14	-0.11	0.915
South-West	urease	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	urease	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	urease	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	urease	CWM_MycInt	Urease	~~	Urease		0.03	0.01	4.90	0.000	0.83	0.10	8.48	0.000
South-West	urease	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	urease	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	urease	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.12	0.07	-1.68	0.094	-0.11	0.06	-1.73	0.083
South-West	urease	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.04	0.30	0.767	0.01	0.04	0.30	0.767
South-West	urease	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.18	0.15	-1.17	0.242	-0.17	0.14	-1.19	0.236
South-West	urease	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.00	0.11	-0.02	0.985	0.00	0.13	-0.02	0.985
South-West	urease	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.18	0.15	-1.17	0.242	-0.17	0.14	-1.19	0.234
South-West	urease	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.00	0.11	-0.01	0.991	0.02	0.13	0.13	0.900
South-West	urease	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	urease	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	urease	Plant_biomass	Urease	~	Plant_biomass	c	-0.09	0.13	-0.70	0.481	-0.10	0.14	-0.71	0.479
South-West	urease	Plant_biomass	Urease	~	LUI_historic	e	-0.18	0.15	-1.18	0.238	-0.17	0.14	-1.20	0.232
South-West	urease	Plant_biomass	Urease	~	LUI_change	f	0.01	0.12	0.06	0.954	0.01	0.14	0.06	0.954
South-West	urease	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	urease	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	urease	Plant_biomass	Urease	~~	Urease		0.04	0.01	5.00	0.000	0.96	0.06	16.87	0.000
South-West	urease	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	urease	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	urease	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.03	-0.60	0.547	-0.02	0.03	-0.61	0.545
South-West	urease	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.27	0.788	0.00	0.02	0.27	0.788
South-West	urease	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.15	-1.31	0.192	-0.18	0.14	-1.33	0.184
South-West	urease	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.01	0.12	0.09	0.931	0.01	0.14	0.09	0.931
South-West	urease	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.20	0.15	-1.31	0.191	-0.19	0.14	-1.36	0.175
South-West	urease	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.01	0.12	0.10	0.923	0.04	0.14	0.28	0.782
South-West	urease	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	urease	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	urease	Lignin_content	Urease	~	Lignin_content	c	0.01	0.11	0.10	0.921	0.01	0.14	0.10	0.921
South-West	urease	Lignin_content	Urease	~	LUI_historic	e	-0.23	0.15	-1.52	0.129	-0.22	0.14	-1.55	0.120
South-West	urease	Lignin_content	Urease	~	LUI_change	f	0.02	0.12	0.15	0.883	0.02	0.14	0.15	0.883
South-West	urease	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	urease	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	urease	Lignin_content	Urease	~~	Urease		0.04	0.01	4.90	0.000	0.95	0.06	15.74	0.000
South-West	urease	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	urease	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	urease	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	0.08	0.937	0.00	0.00	0.08	0.937
South-West	urease	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.10	0.923	0.00	0.01	0.10	0.923
South-West	urease	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.23	0.15	-1.52	0.130	-0.22	0.14	-1.55	0.121
South-West	urease	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.02	0.12	0.16	0.877	0.02	0.14	0.16	0.877
South-West	urease	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.23	0.15	-1.52	0.129	-0.22	0.14	-1.59	0.112
South-West	urease	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.12	0.17	0.867	0.05	0.14	0.36	0.719
South-West	urease	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	urease	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	urease	pH	Urease	~	pH_historic	c	0.03	0.11	0.31	0.758	0.04	0.14	0.31	0.758
South-West	urease	pH	Urease	~	pH_change	d	-0.02	0.14	-0.11	0.917	-0.02	0.14	-0.11	0.917
South-West	urease	pH	Urease	~	LUI_historic	e	-0.19	0.15	-1.27	0.205	-0.18	0.14	-1.29	0.198
South-West	urease	pH	Urease	~	LUI_change	f	0.02	0.12	0.20	0.844	0.03	0.14	0.20	0.844
South-West	urease	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	urease	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	urease	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	urease	pH	Urease	~~	Urease		0.04	0.01	5.00	0.000	0.96	0.05	18.21	0.000
South-West	urease	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	urease	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	urease	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.28	0.780	0.00	0.01	-0.28	0.780
South-West	urease	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.00	0.07	0.948	0.00	0.00	0.07	0.948
South-West	urease	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.15	-1.30	0.193	-0.18	0.14	-1.32	0.186
South-West	urease	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.02	0.12	0.20	0.843	0.03	0.14	0.20	0.843
South-West	urease	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.20	0.15	-1.30	0.192	-0.19	0.14	-1.37	0.171
South-West	urease	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.12	0.21	0.835	0.06	0.14	0.39	0.698

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
South-West	DEA	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	DEA	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	DEA	CWM_leaf_P	DEA	~	CWM_leafP_historic	c	0.34	0.13	2.70	0.007	0.46	0.16	2.82	0.005
South-West	DEA	CWM_leaf_P	DEA	~	CWM_leafP_change	d	0.34	0.13	2.56	0.010	0.30	0.11	2.64	0.008
South-West	DEA	CWM_leaf_P	DEA	~	LUI_historic	e	0.07	0.18	0.37	0.715	0.06	0.17	0.37	0.715
South-West	DEA	CWM_leaf_P	DEA	~	LUI_change	f	0.09	0.10	0.83	0.409	0.10	0.12	0.83	0.407
South-West	DEA	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	DEA	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	DEA	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	DEA	CWM_leaf_P	DEA	~~	DEA		0.03	0.01	4.90	0.000	0.66	0.11	6.11	0.000
South-West	DEA	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	DEA	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	DEA	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.35	0.14	2.53	0.012	0.33	0.12	2.65	0.008
South-West	DEA	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.55	0.579	0.02	0.04	0.56	0.578
South-West	DEA	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.42	0.13	3.10	0.002	0.39	0.12	3.33	0.001
South-West	DEA	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.11	0.11	0.97	0.330	0.12	0.13	0.98	0.328
South-West	DEA	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.42	0.13	3.09	0.002	0.38	0.12	3.18	0.001
South-West	DEA	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.10	0.11	0.96	0.339	0.08	0.14	0.56	0.573
South-West	DEA	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	DEA	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	DEA	CWM_MycInt	DEA	~	CWM_MycInt_historic	c	0.14	0.11	1.30	0.194	0.17	0.13	1.31	0.189
South-West	DEA	CWM_MycInt	DEA	~	CWM_MycInt_change	d	-0.01	0.15	-0.10	0.924	-0.01	0.13	-0.10	0.924
South-West	DEA	CWM_MycInt	DEA	~	LUI_historic	e	0.42	0.14	2.97	0.003	0.39	0.12	3.18	0.001
South-West	DEA	CWM_MycInt	DEA	~	LUI_change	f	0.18	0.12	1.54	0.125	0.20	0.13	1.56	0.120
South-West	DEA	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	DEA	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	DEA	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	DEA	CWM_MycInt	DEA	~~	DEA		0.03	0.01	4.90	0.000	0.76	0.11	7.07	0.000
South-West	DEA	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	DEA	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	DEA	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.05	0.05	1.10	0.270	0.05	0.04	1.12	0.263
South-West	DEA	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.04	-0.10	0.924	0.00	0.04	-0.10	0.924
South-West	DEA	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.48	0.14	3.43	0.001	0.44	0.12	3.79	0.000
South-West	DEA	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.18	0.11	1.58	0.114	0.20	0.13	1.60	0.109
South-West	DEA	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.48	0.14	3.43	0.001	0.42	0.12	3.52	0.000
South-West	DEA	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.17	0.11	1.56	0.119	0.15	0.14	1.07	0.286
South-West	DEA	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	DEA	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	DEA	Plant_biomass	DEA	~	Plant_biomass	c	0.04	0.12	0.33	0.740	0.04	0.13	0.33	0.740
South-West	DEA	Plant_biomass	DEA	~	LUI_historic	e	0.48	0.14	3.46	0.001	0.44	0.12	3.81	0.000
South-West	DEA	Plant_biomass	DEA	~	LUI_change	f	0.18	0.11	1.67	0.095	0.21	0.12	1.70	0.089
South-West	DEA	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	DEA	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	DEA	Plant_biomass	DEA	~~	DEA		0.03	0.01	5.00	0.000	0.78	0.10	7.54	0.000
South-West	DEA	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	DEA	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	DEA	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.32	0.750	0.01	0.02	0.32	0.750
South-West	DEA	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	-0.22	0.827	0.00	0.01	-0.22	0.827
South-West	DEA	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.48	0.14	3.56	0.000	0.45	0.11	3.94	0.000
South-West	DEA	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.18	0.11	1.66	0.097	0.21	0.12	1.68	0.092
South-West	DEA	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.48	0.14	3.55	0.000	0.42	0.12	3.59	0.000
South-West	DEA	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.17	0.11	1.63	0.103	0.14	0.14	1.03	0.301
South-West	DEA	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	DEA	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	DEA	Lignin_content	DEA	~	Lignin_content	c	0.07	0.10	0.68	0.498	0.09	0.13	0.68	0.497
South-West	DEA	Lignin_content	DEA	~	LUI_historic	e	0.46	0.14	3.33	0.001	0.43	0.12	3.65	0.000
South-West	DEA	Lignin_content	DEA	~	LUI_change	f	0.18	0.11	1.65	0.100	0.21	0.13	1.68	0.094
South-West	DEA	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	DEA	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	DEA	Lignin_content	DEA	~~	DEA		0.03	0.01	4.90	0.000	0.78	0.11	7.46	0.000
South-West	DEA	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	DEA	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	DEA	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.13	0.897	0.00	0.01	0.13	0.897
South-West	DEA	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.01	0.42	0.673	0.01	0.02	0.42	0.672
South-West	DEA	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.46	0.14	3.33	0.001	0.43	0.12	3.66	0.000
South-West	DEA	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.18	0.11	1.70	0.090	0.22	0.13	1.73	0.084
South-West	DEA	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.46	0.14	3.32	0.001	0.40	0.12	3.31	0.001
South-West	DEA	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.18	0.11	1.67	0.095	0.16	0.14	1.14	0.255

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
South-West	DEA	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	DEA	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	DEA	pH	DEA	~	pH_historic	c	0.15	0.10	1.50	0.135	0.18	0.12	1.51	0.131
South-West	DEA	pH	DEA	~	pH_change	d	0.09	0.12	0.75	0.451	0.09	0.12	0.76	0.450
South-West	DEA	pH	DEA	~	LUI_historic	e	0.53	0.13	3.93	0.000	0.48	0.11	4.36	0.000
South-West	DEA	pH	DEA	~	LUI_change	f	0.24	0.10	2.27	0.023	0.27	0.12	2.33	0.020
South-West	DEA	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	DEA	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	DEA	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	DEA	pH	DEA	~~	DEA		0.03	0.01	5.00	0.000	0.71	0.11	6.63	0.000
South-West	DEA	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	DEA	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	DEA	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.03	-0.61	0.543	-0.02	0.03	-0.61	0.544
South-West	DEA	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.08	0.934	0.00	0.01	-0.08	0.934
South-West	DEA	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.51	0.14	3.73	0.000	0.46	0.11	4.13	0.000
South-West	DEA	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.24	0.11	2.25	0.025	0.27	0.12	2.31	0.021
South-West	DEA	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.51	0.14	3.72	0.000	0.42	0.12	3.61	0.000
South-West	DEA	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.23	0.11	2.22	0.026	0.21	0.13	1.54	0.124
South-West	phosphatase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	phosphatase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	phosphatase	CWM_leaf_P	Phosphatase	~	CWM_leafP_historic	c	0.17	0.16	1.08	0.283	0.22	0.20	1.09	0.277
South-West	phosphatase	CWM_leaf_P	Phosphatase	~	CWM_leafP_change	d	-0.04	0.17	-0.25	0.800	-0.04	0.14	-0.25	0.800
South-West	phosphatase	CWM_leaf_P	Phosphatase	~	LUI_historic	e	0.01	0.23	0.06	0.951	0.01	0.20	0.06	0.951
South-West	phosphatase	CWM_leaf_P	Phosphatase	~	LUI_change	f	-0.06	0.13	-0.46	0.642	-0.07	0.14	-0.47	0.642
South-West	phosphatase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	phosphatase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	phosphatase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	phosphatase	CWM_leaf_P	Phosphatase	~~	Phosphatase		0.04	0.01	4.90	0.000	0.94	0.07	14.17	0.000
South-West	phosphatase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	phosphatase	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	phosphatase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.18	0.17	1.06	0.288	0.16	0.15	1.08	0.282
South-West	phosphatase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.23	0.817	0.00	0.01	-0.23	0.817
South-West	phosphatase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.19	0.16	1.19	0.235	0.17	0.14	1.21	0.228
South-West	phosphatase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.06	0.13	-0.49	0.627	-0.07	0.14	-0.49	0.626
South-West	phosphatase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.19	0.16	1.19	0.234	0.18	0.14	1.27	0.204
South-West	phosphatase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.06	0.13	-0.49	0.622	-0.09	0.14	-0.62	0.534
South-West	phosphatase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	phosphatase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	phosphatase	CWM_MycInt	Phosphatase	~	CWM_MycInt_historic	c	-0.19	0.13	-1.49	0.137	-0.22	0.14	-1.52	0.129
South-West	phosphatase	CWM_MycInt	Phosphatase	~	CWM_MycInt_change	d	-0.08	0.17	-0.46	0.644	-0.07	0.15	-0.46	0.643
South-West	phosphatase	CWM_MycInt	Phosphatase	~	LUI_historic	e	0.26	0.16	1.56	0.118	0.23	0.14	1.60	0.109
South-West	phosphatase	CWM_MycInt	Phosphatase	~	LUI_change	f	0.01	0.14	0.08	0.935	0.01	0.15	0.08	0.935
South-West	phosphatase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	phosphatase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	phosphatase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	phosphatase	CWM_MycInt	Phosphatase	~~	Phosphatase		0.04	0.01	4.90	0.000	0.93	0.07	12.70	0.000
South-West	phosphatase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	phosphatase	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	phosphatase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.07	0.06	-1.21	0.226	-0.06	0.05	-1.22	0.221
South-West	phosphatase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.04	-0.45	0.651	-0.02	0.05	-0.45	0.650
South-West	phosphatase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.19	0.16	1.16	0.245	0.17	0.14	1.18	0.239
South-West	phosphatase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.01	0.13	-0.06	0.953	-0.01	0.14	-0.06	0.953
South-West	phosphatase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.19	0.16	1.16	0.245	0.17	0.14	1.19	0.233
South-West	phosphatase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.01	0.13	-0.07	0.948	-0.03	0.14	-0.19	0.846
South-West	phosphatase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	phosphatase	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	phosphatase	Plant_biomass	Phosphatase	~	Plant_biomass	c	-0.07	0.14	-0.52	0.602	-0.07	0.14	-0.52	0.601
South-West	phosphatase	Plant_biomass	Phosphatase	~	LUI_historic	e	0.20	0.16	1.24	0.215	0.18	0.14	1.26	0.208
South-West	phosphatase	Plant_biomass	Phosphatase	~	LUI_change	f	-0.03	0.12	-0.22	0.825	-0.03	0.14	-0.22	0.825
South-West	phosphatase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	phosphatase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	phosphatase	Plant_biomass	Phosphatase	~~	Phosphatase		0.04	0.01	5.00	0.000	0.97	0.05	19.05	0.000
South-West	phosphatase	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	phosphatase	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	phosphatase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.48	0.634	-0.01	0.03	-0.48	0.633
South-West	phosphatase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.25	0.799	0.00	0.01	0.25	0.799
South-West	phosphatase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.18	0.16	1.17	0.243	0.16	0.14	1.18	0.237
South-West	phosphatase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.03	0.12	-0.20	0.842	-0.03	0.14	-0.20	0.842
South-West	phosphatase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.19	0.16	1.17	0.243	0.17	0.14	1.23	0.220
South-West	phosphatase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.03	0.12	-0.21	0.834	-0.05	0.14	-0.37	0.710

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
South-West	phosphatase	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	phosphatase	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	phosphatase	Lignin_content	Phosphatase	~	Lignin_content	c	-0.27	0.11	-2.37	0.018	-0.32	0.13	-2.50	0.012
South-West	phosphatase	Lignin_content	Phosphatase	~	LUI_historic	e	0.20	0.15	1.35	0.176	0.18	0.13	1.37	0.170
South-West	phosphatase	Lignin_content	Phosphatase	~	LUI_change	f	0.00	0.12	0.01	0.990	0.00	0.14	0.01	0.990
South-West	phosphatase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	phosphatase	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	phosphatase	Lignin_content	Phosphatase	~~	Phosphatase		0.04	0.01	4.90	0.000	0.87	0.09	9.44	0.000
South-West	phosphatase	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	phosphatase	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	phosphatase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.05	-0.13	0.896	-0.01	0.05	-0.13	0.896
South-West	phosphatase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.02	0.04	-0.53	0.598	-0.03	0.05	-0.53	0.597
South-West	phosphatase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.20	0.16	1.24	0.216	0.18	0.14	1.26	0.209
South-West	phosphatase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.02	0.12	-0.16	0.870	-0.02	0.14	-0.16	0.870
South-West	phosphatase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.20	0.16	1.24	0.216	0.18	0.14	1.29	0.196
South-West	phosphatase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.02	0.12	-0.17	0.863	-0.05	0.14	-0.33	0.739
South-West	phosphatase	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	phosphatase	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	phosphatase	pH	Phosphatase	~	pH_historic	c	-0.66	0.08	-8.31	0.000	-0.72	0.06	-11.21	0.000
South-West	phosphatase	pH	Phosphatase	~	pH_change	d	-0.02	0.10	-0.17	0.869	-0.01	0.09	-0.17	0.869
South-West	phosphatase	pH	Phosphatase	~	LUI_historic	e	0.05	0.11	0.48	0.634	0.04	0.09	0.48	0.635
South-West	phosphatase	pH	Phosphatase	~	LUI_change	f	-0.28	0.08	-3.38	0.001	-0.30	0.09	-3.34	0.001
South-West	phosphatase	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	phosphatase	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	phosphatase	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	phosphatase	pH	Phosphatase	~~	Phosphatase		0.02	0.00	5.00	0.000	0.37	0.08	4.64	0.000
South-West	phosphatase	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	phosphatase	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	phosphatase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.08	0.13	0.66	0.507	0.07	0.10	0.67	0.503
South-West	phosphatase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.00	0.08	0.941	0.00	0.00	0.08	0.941
South-West	phosphatase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.13	0.16	0.82	0.414	0.11	0.13	0.82	0.410
South-West	phosphatase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.28	0.08	-3.38	0.001	-0.30	0.09	-3.33	0.001
South-West	phosphatase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.14	0.16	0.83	0.408	0.15	0.14	1.11	0.268
South-West	phosphatase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.28	0.08	-3.39	0.001	-0.31	0.09	-3.49	0.000
South-West	bacteria	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	bacteria	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	bacteria	CWM_leaf_P	bactotal	~	CWM_leafP_historic	c	0.14	0.15	0.89	0.373	0.18	0.20	0.90	0.370
South-West	bacteria	CWM_leaf_P	bactotal	~	CWM_leafP_change	d	0.11	0.16	0.65	0.517	0.09	0.14	0.65	0.515
South-West	bacteria	CWM_leaf_P	bactotal	~	LUI_historic	e	-0.05	0.22	-0.22	0.828	-0.04	0.20	-0.22	0.828
South-West	bacteria	CWM_leaf_P	bactotal	~	LUI_change	f	-0.16	0.13	-1.23	0.217	-0.17	0.14	-1.25	0.210
South-West	bacteria	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	bacteria	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	bacteria	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	bacteria	CWM_leaf_P	bactotal	~~	bactotal		0.04	0.01	4.90	0.000	0.94	0.07	13.96	0.000
South-West	bacteria	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	bacteria	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	bacteria	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.14	0.16	0.88	0.377	0.13	0.15	0.89	0.373
South-West	bacteria	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.02	0.43	0.669	0.01	0.02	0.43	0.669
South-West	bacteria	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.09	0.16	0.61	0.545	0.09	0.14	0.61	0.544
South-West	bacteria	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.15	0.13	-1.18	0.238	-0.17	0.14	-1.20	0.231
South-West	bacteria	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.10	0.16	0.61	0.542	0.11	0.14	0.74	0.460
South-West	bacteria	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.15	0.13	-1.19	0.236	-0.18	0.14	-1.27	0.203
South-West	bacteria	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	bacteria	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	bacteria	CWM_MycInt	bactotal	~	CWM_MycInt_historic	c	-0.17	0.12	-1.45	0.147	-0.21	0.14	-1.48	0.140
South-West	bacteria	CWM_MycInt	bactotal	~	CWM_MycInt_change	d	0.10	0.16	0.58	0.563	0.08	0.15	0.58	0.562
South-West	bacteria	CWM_MycInt	bactotal	~	LUI_historic	e	0.19	0.16	1.20	0.232	0.17	0.14	1.21	0.226
South-West	bacteria	CWM_MycInt	bactotal	~	LUI_change	f	-0.12	0.13	-0.94	0.346	-0.14	0.15	-0.95	0.342
South-West	bacteria	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	bacteria	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	bacteria	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	bacteria	CWM_MycInt	bactotal	~~	bactotal		0.04	0.01	4.90	0.000	0.92	0.07	12.68	0.000
South-West	bacteria	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	bacteria	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	bacteria	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.07	0.06	-1.19	0.234	-0.06	0.05	-1.20	0.229
South-West	bacteria	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.56	0.576	0.03	0.05	0.56	0.575
South-West	bacteria	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.12	0.16	0.80	0.425	0.11	0.14	0.80	0.422
South-West	bacteria	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.10	0.12	-0.80	0.421	-0.11	0.14	-0.81	0.419
South-West	bacteria	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.12	0.15	0.80	0.423	0.13	0.14	0.90	0.370
South-West	bacteria	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.12	-0.81	0.418	-0.13	0.14	-0.90	0.366

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
South-West	bacteria	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	bacteria	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	bacteria	Plant_biomass	bactotal	~	Plant_biomass	c	-0.08	0.13	-0.62	0.537	-0.09	0.14	-0.62	0.536
South-West	bacteria	Plant_biomass	bactotal	~	LUI_historic	e	0.12	0.16	0.76	0.449	0.11	0.14	0.76	0.447
South-West	bacteria	Plant_biomass	bactotal	~	LUI_change	f	-0.10	0.12	-0.82	0.412	-0.12	0.14	-0.83	0.409
South-West	bacteria	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	bacteria	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	bacteria	Plant_biomass	bactotal	~~	bactotal		0.04	0.01	5.00	0.000	0.97	0.05	19.84	0.000
South-West	bacteria	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	bacteria	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	bacteria	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.03	-0.55	0.585	-0.01	0.03	-0.55	0.584
South-West	bacteria	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.26	0.792	0.00	0.01	0.26	0.792
South-West	bacteria	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.10	0.16	0.66	0.508	0.09	0.14	0.67	0.506
South-West	bacteria	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.10	0.12	-0.79	0.428	-0.11	0.14	-0.80	0.425
South-West	bacteria	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.10	0.16	0.67	0.505	0.11	0.14	0.79	0.431
South-West	bacteria	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.12	-0.80	0.424	-0.13	0.14	-0.90	0.366
South-West	bacteria	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	bacteria	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	bacteria	Lignin_content	bactotal	~	Lignin_content	c	-0.12	0.12	-0.98	0.326	-0.14	0.14	-0.99	0.321
South-West	bacteria	Lignin_content	bactotal	~	LUI_historic	e	0.10	0.16	0.64	0.525	0.09	0.14	0.64	0.524
South-West	bacteria	Lignin_content	bactotal	~	LUI_change	f	-0.08	0.12	-0.68	0.494	-0.10	0.14	-0.69	0.492
South-West	bacteria	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	bacteria	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	bacteria	Lignin_content	bactotal	~~	bactotal		0.04	0.01	4.90	0.000	0.96	0.06	17.00	0.000
South-West	bacteria	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	bacteria	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	bacteria	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.13	0.896	0.00	0.02	-0.13	0.896
South-West	bacteria	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.02	-0.47	0.636	-0.01	0.02	-0.48	0.635
South-West	bacteria	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.10	0.16	0.61	0.541	0.09	0.14	0.61	0.540
South-West	bacteria	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.09	0.12	-0.76	0.450	-0.11	0.14	-0.76	0.448
South-West	bacteria	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.10	0.16	0.62	0.539	0.10	0.14	0.72	0.470
South-West	bacteria	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.12	-0.76	0.447	-0.12	0.14	-0.85	0.395
South-West	bacteria	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	bacteria	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	bacteria	pH	bactotal	~	pH_historic	c	-0.20	0.11	-1.87	0.062	-0.24	0.13	-1.92	0.055
South-West	bacteria	pH	bactotal	~	pH_change	d	0.21	0.14	1.57	0.116	0.20	0.13	1.60	0.109
South-West	bacteria	pH	bactotal	~	LUI_historic	e	0.09	0.15	0.62	0.536	0.08	0.13	0.62	0.535
South-West	bacteria	pH	bactotal	~	LUI_change	f	-0.17	0.12	-1.48	0.138	-0.20	0.13	-1.51	0.132
South-West	bacteria	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	bacteria	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	bacteria	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	bacteria	pH	bactotal	~~	bactotal		0.04	0.01	5.00	0.000	0.84	0.09	9.09	0.000
South-West	bacteria	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	bacteria	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	bacteria	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.04	0.63	0.531	0.02	0.04	0.63	0.528
South-West	bacteria	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.03	-0.08	0.933	0.00	0.03	-0.08	0.933
South-West	bacteria	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.12	0.15	0.77	0.442	0.10	0.14	0.77	0.439
South-West	bacteria	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.17	0.12	-1.47	0.143	-0.20	0.13	-1.49	0.135
South-West	bacteria	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.12	0.15	0.78	0.437	0.13	0.14	0.98	0.326
South-West	bacteria	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.17	0.12	-1.47	0.141	-0.21	0.13	-1.62	0.105
South-West	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	CWM_leafP_historic	c	-0.42	0.16	-2.65	0.008	-0.49	0.17	-2.81	0.005
South-West	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	CWM_leafP_change	d	-0.19	0.17	-1.15	0.249	-0.15	0.13	-1.16	0.246
South-West	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	LUI_historic	e	0.06	0.23	0.27	0.784	0.05	0.18	0.28	0.784
South-West	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	LUI_change	f	0.03	0.13	0.24	0.808	0.03	0.13	0.24	0.808
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~~	fungi_bac		0.04	0.01	4.90	0.000	0.77	0.11	7.36	0.000
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.43	0.17	-2.49	0.013	-0.35	0.13	-2.63	0.009
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.02	-0.51	0.611	-0.01	0.02	-0.51	0.610
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.37	0.17	-2.19	0.028	-0.30	0.13	-2.30	0.022
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.02	0.13	0.15	0.883	0.02	0.13	0.15	0.883
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.37	0.17	-2.20	0.028	-0.30	0.13	-2.33	0.020
South-West	fungi:bacteria ratio	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.13	0.16	0.872	0.05	0.14	0.40	0.692

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
South-West	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	CWM_MycInt_historic	c	0.11	0.13	0.84	0.401	0.12	0.14	0.85	0.398
South-West	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	CWM_MycInt_change	d	0.20	0.18	1.12	0.263	0.16	0.14	1.13	0.258
South-West	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	LUI_historic	e	-0.44	0.17	-2.55	0.011	-0.36	0.13	-2.71	0.007
South-West	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	LUI_change	f	-0.14	0.14	-0.96	0.337	-0.14	0.14	-0.97	0.334
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~~	fungi_bac		0.05	0.01	4.90	0.000	0.86	0.09	9.29	0.000
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.04	0.05	0.78	0.436	0.03	0.04	0.78	0.434
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.05	0.05	1.00	0.319	0.05	0.05	1.00	0.315
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.40	0.17	-2.40	0.017	-0.33	0.13	-2.53	0.011
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.09	0.14	-0.65	0.518	-0.09	0.14	-0.65	0.517
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.40	0.17	-2.40	0.017	-0.32	0.13	-2.45	0.014
South-West	fungi:bacteria ratio	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.14	-0.63	0.527	-0.05	0.14	-0.35	0.724
South-West	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	Plant_biomass	c	-0.01	0.14	-0.04	0.969	-0.01	0.14	-0.04	0.969
South-West	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	LUI_historic	e	-0.41	0.17	-2.46	0.014	-0.34	0.13	-2.60	0.009
South-West	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	LUI_change	f	-0.08	0.13	-0.63	0.531	-0.09	0.13	-0.63	0.529
South-West	fungi:bacteria ratio	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	fungi:bacteria ratio	Plant_biomass	fungi_bac	~~	fungi_bac		0.04	0.01	5.00	0.000	0.89	0.08	10.57	0.000
South-West	fungi:bacteria ratio	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.03	-0.04	0.969	0.00	0.02	-0.04	0.969
South-West	fungi:bacteria ratio	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.04	0.969	0.00	0.01	0.04	0.969
South-West	fungi:bacteria ratio	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.41	0.17	-2.50	0.013	-0.34	0.13	-2.65	0.008
South-West	fungi:bacteria ratio	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.08	0.13	-0.63	0.531	-0.08	0.13	-0.63	0.530
South-West	fungi:bacteria ratio	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.41	0.17	-2.50	0.013	-0.32	0.13	-2.56	0.010
South-West	fungi:bacteria ratio	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.08	0.13	-0.61	0.544	-0.04	0.14	-0.25	0.806
South-West	fungi:bacteria ratio	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	fungi:bacteria ratio	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	fungi:bacteria ratio	Lignin_content	fungi_bac	~	Lignin_content	c	-0.07	0.13	-0.56	0.573	-0.08	0.14	-0.57	0.572
South-West	fungi:bacteria ratio	Lignin_content	fungi_bac	~	LUI_historic	e	-0.40	0.17	-2.38	0.017	-0.33	0.13	-2.51	0.012
South-West	fungi:bacteria ratio	Lignin_content	fungi_bac	~	LUI_change	f	-0.08	0.13	-0.64	0.521	-0.09	0.14	-0.64	0.520
South-West	fungi:bacteria ratio	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	fungi:bacteria ratio	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	fungi:bacteria ratio	Lignin_content	fungi_bac	~~	fungi_bac		0.05	0.01	4.90	0.000	0.89	0.09	10.27	0.000
South-West	fungi:bacteria ratio	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.13	0.898	0.00	0.01	-0.13	0.898
South-West	fungi:bacteria ratio	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.02	-0.39	0.696	-0.01	0.02	-0.39	0.696
South-West	fungi:bacteria ratio	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.40	0.17	-2.38	0.017	-0.33	0.13	-2.52	0.012
South-West	fungi:bacteria ratio	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.09	0.13	-0.69	0.493	-0.09	0.14	-0.69	0.491
South-West	fungi:bacteria ratio	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.40	0.17	-2.38	0.017	-0.32	0.13	-2.42	0.015
South-West	fungi:bacteria ratio	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.13	-0.67	0.504	-0.05	0.14	-0.34	0.734
South-West	fungi:bacteria ratio	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	fungi:bacteria ratio	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	fungi:bacteria ratio	pH	fungi_bac	~	pH_historic	c	0.21	0.12	1.80	0.073	0.23	0.13	1.84	0.066
South-West	fungi:bacteria ratio	pH	fungi_bac	~	pH_change	d	-0.16	0.15	-1.09	0.278	-0.14	0.13	-1.09	0.274
South-West	fungi:bacteria ratio	pH	fungi_bac	~	LUI_historic	e	-0.39	0.16	-2.46	0.014	-0.32	0.12	-2.58	0.010
South-West	fungi:bacteria ratio	pH	fungi_bac	~	LUI_change	f	0.00	0.12	-0.02	0.984	0.00	0.13	-0.02	0.984
South-West	fungi:bacteria ratio	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	fungi:bacteria ratio	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	fungi:bacteria ratio	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	fungi:bacteria ratio	pH	fungi_bac	~~	fungi_bac		0.04	0.01	5.00	0.000	0.81	0.10	8.24	0.000
South-West	fungi:bacteria ratio	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi:bacteria ratio	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.03	0.04	-0.62	0.532	-0.02	0.03	-0.63	0.529
South-West	fungi:bacteria ratio	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.02	0.08	0.934	0.00	0.02	0.08	0.934
South-West	fungi:bacteria ratio	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.42	0.16	-2.56	0.010	-0.34	0.13	-2.72	0.007
South-West	fungi:bacteria ratio	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.00	0.13	-0.01	0.994	0.00	0.13	-0.01	0.994
South-West	fungi:bacteria ratio	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.42	0.16	-2.56	0.010	-0.34	0.12	-2.75	0.006
South-West	fungi:bacteria ratio	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.00	0.13	0.01	0.990	0.05	0.14	0.36	0.721

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
South-West	fungi	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	fungi	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	fungi	CWM_leaf_P	fungi	~	CWM_leafP_historic	c	-0.26	0.15	-1.72	0.086	-0.34	0.19	-1.76	0.078
South-West	fungi	CWM_leaf_P	fungi	~	CWM_leafP_change	d	-0.18	0.16	-1.10	0.271	-0.15	0.13	-1.11	0.266
South-West	fungi	CWM_leaf_P	fungi	~	LUI_historic	e	0.18	0.22	0.82	0.411	0.16	0.20	0.83	0.408
South-West	fungi	CWM_leaf_P	fungi	~	LUI_change	f	-0.18	0.13	-1.41	0.158	-0.19	0.13	-1.44	0.151
South-West	fungi	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	fungi	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	fungi	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	fungi	CWM_leaf_P	fungi	~~	fungi		0.04	0.01	4.90	0.000	0.88	0.09	10.11	0.000
South-West	fungi	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.27	0.16	-1.67	0.095	-0.24	0.14	-1.71	0.087
South-West	fungi	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.02	-0.51	0.614	-0.01	0.02	-0.51	0.612
South-West	fungi	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.09	0.16	-0.58	0.564	-0.08	0.14	-0.58	0.563
South-West	fungi	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.19	0.13	-1.49	0.137	-0.21	0.14	-1.52	0.129
South-West	fungi	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.09	0.16	-0.57	0.568	-0.06	0.14	-0.40	0.688
South-West	fungi	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.19	0.13	-1.49	0.137	-0.20	0.14	-1.45	0.147
South-West	fungi	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	fungi	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	fungi	CWM_MycInt	fungi	~	CWM_MycInt_historic	c	0.05	0.12	0.38	0.706	0.05	0.14	0.38	0.706
South-West	fungi	CWM_MycInt	fungi	~	CWM_MycInt_change	d	0.31	0.17	1.88	0.060	0.26	0.14	1.93	0.053
South-West	fungi	CWM_MycInt	fungi	~	LUI_historic	e	-0.13	0.16	-0.78	0.433	-0.11	0.14	-0.79	0.431
South-West	fungi	CWM_MycInt	fungi	~	LUI_change	f	-0.33	0.13	-2.50	0.013	-0.35	0.13	-2.63	0.008
South-West	fungi	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	fungi	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	fungi	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	fungi	CWM_MycInt	fungi	~~	fungi		0.04	0.01	4.90	0.000	0.86	0.09	9.19	0.000
South-West	fungi	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.05	0.37	0.711	0.02	0.04	0.37	0.711
South-West	fungi	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.07	0.05	1.43	0.154	0.08	0.06	1.44	0.151
South-West	fungi	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.11	0.15	-0.70	0.481	-0.10	0.13	-0.71	0.480
South-West	fungi	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.25	0.13	-1.96	0.050	-0.27	0.13	-2.03	0.042
South-West	fungi	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.11	0.15	-0.70	0.486	-0.06	0.14	-0.46	0.649
South-West	fungi	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.25	0.13	-1.95	0.051	-0.26	0.13	-1.95	0.051
South-West	fungi	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	fungi	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	fungi	Plant_biomass	fungi	~	Plant_biomass	c	-0.04	0.13	-0.31	0.759	-0.04	0.14	-0.31	0.759
South-West	fungi	Plant_biomass	fungi	~	LUI_historic	e	-0.13	0.16	-0.80	0.425	-0.11	0.14	-0.80	0.422
South-West	fungi	Plant_biomass	fungi	~	LUI_change	f	-0.24	0.12	-1.94	0.052	-0.27	0.13	-2.01	0.044
South-West	fungi	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	fungi	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	fungi	Plant_biomass	fungi	~~	fungi		0.04	0.01	5.00	0.000	0.92	0.07	12.76	0.000
South-West	fungi	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.30	0.767	-0.01	0.02	-0.30	0.767
South-West	fungi	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.21	0.833	0.00	0.01	0.21	0.833
South-West	fungi	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.15	-0.86	0.391	-0.12	0.14	-0.86	0.388
South-West	fungi	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.23	0.12	-1.93	0.054	-0.27	0.13	-2.00	0.046
South-West	fungi	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.13	0.15	-0.85	0.396	-0.08	0.14	-0.56	0.574
South-West	fungi	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.23	0.12	-1.92	0.054	-0.25	0.13	-1.87	0.062
South-West	fungi	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	fungi	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	fungi	Lignin_content	fungi	~	Lignin_content	c	-0.09	0.12	-0.71	0.477	-0.10	0.14	-0.72	0.475
South-West	fungi	Lignin_content	fungi	~	LUI_historic	e	-0.14	0.16	-0.87	0.386	-0.12	0.14	-0.87	0.383
South-West	fungi	Lignin_content	fungi	~	LUI_change	f	-0.23	0.12	-1.84	0.066	-0.26	0.14	-1.90	0.057
South-West	fungi	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	fungi	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	fungi	Lignin_content	fungi	~~	fungi		0.04	0.01	4.90	0.000	0.91	0.08	11.82	0.000
South-West	fungi	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	fungi	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.13	0.897	0.00	0.02	-0.13	0.897
South-West	fungi	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.02	-0.43	0.667	-0.01	0.02	-0.43	0.666
South-West	fungi	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.14	0.16	-0.88	0.381	-0.12	0.14	-0.88	0.378
South-West	fungi	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.23	0.12	-1.89	0.059	-0.27	0.14	-1.96	0.050
South-West	fungi	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.14	0.16	-0.87	0.385	-0.09	0.14	-0.60	0.548
South-West	fungi	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.23	0.12	-1.89	0.059	-0.25	0.14	-1.83	0.067

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
South-West	fungi	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	fungi	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	fungi	pH	fungi	~	pH_historic	c	0.11	0.11	0.94	0.348	0.13	0.14	0.95	0.344
South-West	fungi	pH	fungi	~	pH_change	d	0.00	0.14	0.01	0.991	0.00	0.14	0.01	0.991
South-West	fungi	pH	fungi	~	LUI_historic	e	-0.11	0.15	-0.72	0.471	-0.10	0.14	-0.73	0.468
South-West	fungi	pH	fungi	~	LUI_change	f	-0.19	0.12	-1.59	0.111	-0.22	0.14	-1.63	0.103
South-West	fungi	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	fungi	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	fungi	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.94	0.000
South-West	fungi	pH	fungi	~~	fungi		0.04	0.01	5.00	0.000	0.93	0.07	13.43	0.000
South-West	fungi	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	fungi	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.54	0.587	-0.01	0.02	-0.55	0.586
South-West	fungi	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.00	-0.01	0.991	0.00	0.00	-0.01	0.991
South-West	fungi	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.12	0.15	-0.81	0.421	-0.11	0.14	-0.81	0.418
South-West	fungi	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.19	0.12	-1.60	0.111	-0.22	0.14	-1.63	0.103
South-West	fungi	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.12	0.15	-0.80	0.425	-0.08	0.14	-0.57	0.571
South-West	fungi	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.19	0.12	-1.59	0.112	-0.20	0.13	-1.51	0.131
South-West	ergosterol	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	1.04	0.14	7.23	0.000	0.72	0.07	10.44	0.000
South-West	ergosterol	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	0.06	0.11	0.57	0.570	0.08	0.14	0.57	0.569
South-West	ergosterol	CWM_leaf_P	Ergosterol	~	CWM_leafP_historic	c	-0.41	0.16	-2.59	0.010	-0.47	0.17	-2.71	0.007
South-West	ergosterol	CWM_leaf_P	Ergosterol	~	CWM_leafP_change	d	0.00	0.17	0.00	0.997	0.00	0.13	0.00	0.997
South-West	ergosterol	CWM_leaf_P	Ergosterol	~	LUI_historic	e	0.18	0.23	0.78	0.438	0.14	0.18	0.78	0.437
South-West	ergosterol	CWM_leaf_P	Ergosterol	~	LUI_change	f	-0.37	0.13	-2.86	0.004	-0.36	0.12	-3.02	0.003
South-West	ergosterol	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	ergosterol	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.48	0.10	4.80	0.000
South-West	ergosterol	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.03	0.01	4.90	0.000	0.99	0.02	42.42	0.000
South-West	ergosterol	CWM_leaf_P	Ergosterol	~~	Ergosterol		0.04	0.01	4.90	0.000	0.74	0.11	7.03	0.000
South-West	ergosterol	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	ergosterol	CWM_leaf_P	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	ergosterol	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.43	0.18	-2.44	0.015	-0.34	0.13	-2.54	0.011
South-West	ergosterol	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.00	0.997	0.00	0.01	0.00	0.997
South-West	ergosterol	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.25	0.17	-1.47	0.141	-0.20	0.13	-1.49	0.135
South-West	ergosterol	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.37	0.13	-2.87	0.004	-0.36	0.12	-3.03	0.002
South-West	ergosterol	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.25	0.17	-1.46	0.144	-0.16	0.14	-1.10	0.271
South-West	ergosterol	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.37	0.13	-2.86	0.004	-0.34	0.12	-2.78	0.005
South-West	ergosterol	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.38	0.18	2.09	0.037	0.29	0.13	2.18	0.029
South-West	ergosterol	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.24	0.11	2.18	0.029	0.30	0.13	2.29	0.022
South-West	ergosterol	CWM_MycInt	Ergosterol	~	CWM_MycInt_historic	c	-0.08	0.13	-0.63	0.527	-0.08	0.13	-0.63	0.527
South-West	ergosterol	CWM_MycInt	Ergosterol	~	CWM_MycInt_change	d	0.30	0.18	1.72	0.086	0.22	0.13	1.74	0.081
South-West	ergosterol	CWM_MycInt	Ergosterol	~	LUI_historic	e	-0.21	0.17	-1.26	0.209	-0.16	0.13	-1.27	0.205
South-West	ergosterol	CWM_MycInt	Ergosterol	~	LUI_change	f	-0.53	0.14	-3.82	0.000	-0.50	0.12	-4.27	0.000
South-West	ergosterol	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.80	0.426	-0.12	0.14	-0.81	0.417
South-West	ergosterol	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.92	0.08	12.02	0.000
South-West	ergosterol	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	0.91	0.08	11.52	0.000
South-West	ergosterol	CWM_MycInt	Ergosterol	~~	Ergosterol		0.04	0.01	4.90	0.000	0.74	0.11	6.88	0.000
South-West	ergosterol	CWM_MycInt	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	ergosterol	CWM_MycInt	LUI_change	~~	LUI_change		0.05	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	ergosterol	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.03	0.05	-0.61	0.545	-0.02	0.04	-0.61	0.544
South-West	ergosterol	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.07	0.05	1.35	0.177	0.07	0.05	1.35	0.176
South-West	ergosterol	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.24	0.16	-1.49	0.135	-0.19	0.12	-1.51	0.130
South-West	ergosterol	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.46	0.14	-3.37	0.001	-0.43	0.12	-3.71	0.000
South-West	ergosterol	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.24	0.16	-1.48	0.139	-0.14	0.14	-1.00	0.320
South-West	ergosterol	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.46	0.14	-3.36	0.001	-0.41	0.12	-3.46	0.001
South-West	ergosterol	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.16	1.17	0.244	0.16	0.14	1.18	0.238
South-West	ergosterol	Plant_biomass	Plant_biomass	~	LUI_change	b	-0.04	0.13	-0.29	0.771	-0.04	0.14	-0.29	0.771
South-West	ergosterol	Plant_biomass	Ergosterol	~	Plant_biomass	c	0.09	0.15	0.61	0.545	0.08	0.13	0.61	0.544
South-West	ergosterol	Plant_biomass	Ergosterol	~	LUI_historic	e	-0.30	0.17	-1.75	0.080	-0.23	0.13	-1.79	0.074
South-West	ergosterol	Plant_biomass	Ergosterol	~	LUI_change	f	-0.40	0.13	-3.02	0.003	-0.39	0.12	-3.25	0.001
South-West	ergosterol	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	ergosterol	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	5.00	0.000	0.97	0.05	20.22	0.000
South-West	ergosterol	Plant_biomass	Ergosterol	~~	Ergosterol		0.05	0.01	5.00	0.000	0.82	0.10	8.27	0.000
South-West	ergosterol	Plant_biomass	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	ergosterol	Plant_biomass	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	ergosterol	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.03	0.54	0.591	0.01	0.02	0.54	0.591
South-West	ergosterol	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	-0.26	0.793	0.00	0.01	-0.26	0.793
South-West	ergosterol	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.28	0.17	-1.67	0.095	-0.22	0.13	-1.70	0.089
South-West	ergosterol	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.41	0.13	-3.03	0.002	-0.39	0.12	-3.28	0.001
South-West	ergosterol	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.28	0.17	-1.66	0.098	-0.16	0.14	-1.15	0.250
South-West	ergosterol	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.40	0.13	-3.02	0.003	-0.36	0.12	-2.94	0.003

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P*.std
South-West	ergosterol	Lignin_content	Lignin_content	~	LUI_historic	a	0.03	0.19	0.13	0.895	0.02	0.15	0.13	0.895
South-West	ergosterol	Lignin_content	Lignin_content	~	LUI_change	b	0.08	0.15	0.54	0.589	0.08	0.15	0.54	0.588
South-West	ergosterol	Lignin_content	Ergosterol	~	Lignin_content	c	-0.20	0.13	-1.57	0.117	-0.20	0.13	-1.60	0.111
South-West	ergosterol	Lignin_content	Ergosterol	~	LUI_historic	e	-0.28	0.17	-1.64	0.100	-0.21	0.13	-1.67	0.095
South-West	ergosterol	Lignin_content	Ergosterol	~	LUI_change	f	-0.39	0.13	-2.91	0.004	-0.38	0.12	-3.11	0.002
South-West	ergosterol	Lignin_content	LUI_historic	~~	LUI_change	g	-0.01	0.01	-0.95	0.342	-0.14	0.14	-0.98	0.329
South-West	ergosterol	Lignin_content	Lignin_content	~~	Lignin_content		0.06	0.01	4.90	0.000	0.99	0.02	44.29	0.000
South-West	ergosterol	Lignin_content	Ergosterol	~~	Ergosterol		0.05	0.01	4.90	0.000	0.78	0.11	7.44	0.000
South-West	ergosterol	Lignin_content	LUI_historic	~~	LUI_historic		0.03	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	ergosterol	Lignin_content	LUI_change	~~	LUI_change		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
South-West	ergosterol	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.04	-0.13	0.896	0.00	0.03	-0.13	0.896
South-West	ergosterol	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.02	0.03	-0.51	0.609	-0.02	0.03	-0.52	0.607
South-West	ergosterol	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.29	0.18	-1.63	0.103	-0.22	0.13	-1.66	0.096
South-West	ergosterol	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.41	0.14	-2.97	0.003	-0.39	0.12	-3.20	0.001
South-West	ergosterol	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.28	0.18	-1.62	0.106	-0.16	0.14	-1.15	0.251
South-West	ergosterol	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.40	0.14	-2.96	0.003	-0.36	0.13	-2.89	0.004
South-West	ergosterol	pH	pH_historic	~	LUI_historic	a	-0.13	0.19	-0.67	0.505	-0.09	0.14	-0.67	0.504
South-West	ergosterol	pH	pH_change	~	LUI_change	b	-0.01	0.12	-0.08	0.933	-0.01	0.14	-0.08	0.933
South-West	ergosterol	pH	Ergosterol	~	pH_historic	c	0.16	0.13	1.25	0.211	0.16	0.13	1.26	0.206
South-West	ergosterol	pH	Ergosterol	~	pH_change	d	-0.02	0.16	-0.12	0.901	-0.02	0.13	-0.12	0.901
South-West	ergosterol	pH	Ergosterol	~	LUI_historic	e	-0.26	0.17	-1.52	0.129	-0.20	0.13	-1.54	0.123
South-West	ergosterol	pH	Ergosterol	~	LUI_change	f	-0.34	0.13	-2.62	0.009	-0.34	0.12	-2.77	0.006
South-West	ergosterol	pH	LUI_historic	~~	LUI_change	g	-0.01	0.01	-1.03	0.303	-0.15	0.14	-1.07	0.287
South-West	ergosterol	pH	pH_historic	~~	pH_historic		0.06	0.01	5.00	0.000	0.99	0.03	37.71	0.000
South-West	ergosterol	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	1.00	0.00	298.93	0.000
South-West	ergosterol	pH	Ergosterol	~~	Ergosterol		0.05	0.01	5.00	0.000	0.83	0.10	8.73	0.000
South-West	ergosterol	pH	LUI_historic	~~	LUI_historic		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	ergosterol	pH	LUI_change	~~	LUI_change		0.05	0.01	5.00	0.000	1.00	0.00	NA	NA
South-West	ergosterol	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.03	-0.59	0.557	-0.02	0.03	-0.59	0.555
South-West	ergosterol	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.00	0.07	0.945	0.00	0.00	0.07	0.945
South-West	ergosterol	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.28	0.17	-1.62	0.106	-0.21	0.13	-1.65	0.099
South-West	ergosterol	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.34	0.13	-2.61	0.009	-0.34	0.12	-2.76	0.006
South-West	ergosterol	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.27	0.17	-1.61	0.109	-0.16	0.14	-1.19	0.234
South-West	ergosterol	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.34	0.13	-2.60	0.009	-0.31	0.13	-2.45	0.014
Central	Cmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	Cmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	Cmic	CWM_leaf_P	Cmic	~	CWM_leafP_historic	c	-0.13	0.18	-0.72	0.472	-0.13	0.17	-0.72	0.470
Central	Cmic	CWM_leaf_P	Cmic	~	CWM_leafP_change	d	0.06	0.20	0.27	0.785	0.04	0.14	0.27	0.785
Central	Cmic	CWM_leaf_P	Cmic	~	LUI_historic	e	-0.18	0.15	-1.16	0.248	-0.20	0.17	-1.17	0.242
Central	Cmic	CWM_leaf_P	Cmic	~	LUI_change	f	0.03	0.15	0.21	0.833	0.03	0.14	0.21	0.833
Central	Cmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	Cmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	Cmic	CWM_leaf_P	Cmic	~~	Cmic		0.05	0.01	5.00	0.000	0.91	0.08	11.77	0.000
Central	Cmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.07	0.10	-0.71	0.475	-0.08	0.11	-0.72	0.473
Central	Cmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.23	0.815	0.00	0.01	-0.24	0.815
Central	Cmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.24	0.12	-2.08	0.038	-0.28	0.13	-2.17	0.030
Central	Cmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.03	0.15	0.19	0.846	0.03	0.14	0.19	0.846
Central	Cmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.24	0.12	-2.08	0.038	-0.28	0.13	-2.16	0.031
Central	Cmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.03	0.15	0.19	0.850	0.01	0.14	0.06	0.954
Central	Cmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	Cmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	Cmic	CWM_MycInt	Cmic	~	CWM_MycInt_historic	c	0.15	0.13	1.16	0.247	0.15	0.13	1.17	0.242
Central	Cmic	CWM_MycInt	Cmic	~	CWM_MycInt_change	d	0.10	0.16	0.58	0.562	0.08	0.13	0.58	0.561
Central	Cmic	CWM_MycInt	Cmic	~	LUI_historic	e	-0.26	0.12	-2.18	0.029	-0.29	0.13	-2.27	0.023
Central	Cmic	CWM_MycInt	Cmic	~	LUI_change	f	0.01	0.15	0.07	0.947	0.01	0.13	0.07	0.947
Central	Cmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	Cmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	Cmic	CWM_MycInt	Cmic	~~	Cmic		0.04	0.01	5.00	0.000	0.88	0.09	10.03	0.000
Central	Cmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.02	-0.70	0.484	-0.02	0.03	-0.71	0.481
Central	Cmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.26	0.792	0.00	0.01	0.26	0.792
Central	Cmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.27	0.12	-2.31	0.021	-0.31	0.13	-2.43	0.015
Central	Cmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.01	0.15	0.09	0.928	0.01	0.13	0.09	0.928
Central	Cmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.27	0.12	-2.31	0.021	-0.31	0.13	-2.42	0.015
Central	Cmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.01	0.15	0.09	0.933	-0.01	0.14	-0.06	0.956

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
Central	Cmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	Cmic	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	Cmic	Plant_biomass	Cmic	~	Plant_biomass	c	0.14	0.14	0.98	0.325	0.13	0.13	0.99	0.321
Central	Cmic	Plant_biomass	Cmic	~	LUI_historic	e	-0.25	0.12	-2.13	0.033	-0.29	0.13	-2.22	0.026
Central	Cmic	Plant_biomass	Cmic	~	LUI_change	f	0.01	0.15	0.05	0.964	0.01	0.14	0.05	0.964
Central	Cmic	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	Cmic	Plant_biomass	Cmic	~~	Cmic		0.05	0.01	5.00	0.000	0.90	0.08	11.35	0.000
Central	Cmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.22	0.825	0.00	0.02	0.22	0.825
Central	Cmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.03	0.65	0.515	0.02	0.03	0.65	0.513
Central	Cmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.25	0.12	-2.08	0.038	-0.28	0.13	-2.17	0.030
Central	Cmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.03	0.15	0.17	0.869	0.02	0.14	0.17	0.869
Central	Cmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.25	0.12	-2.08	0.038	-0.28	0.13	-2.16	0.031
Central	Cmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.15	0.16	0.873	0.00	0.14	0.03	0.976
Central	Cmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	Cmic	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	Cmic	Lignin_content	Cmic	~	Lignin_content	c	0.05	0.14	0.38	0.702	0.05	0.14	0.38	0.702
Central	Cmic	Lignin_content	Cmic	~	LUI_historic	e	-0.25	0.12	-2.11	0.035	-0.29	0.13	-2.20	0.028
Central	Cmic	Lignin_content	Cmic	~	LUI_change	f	0.02	0.15	0.14	0.889	0.02	0.14	0.14	0.889
Central	Cmic	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	Cmic	Lignin_content	Cmic	~~	Cmic		0.05	0.01	5.00	0.000	0.92	0.07	12.32	0.000
Central	Cmic	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.32	0.747	0.00	0.01	0.32	0.747
Central	Cmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.30	0.768	0.00	0.01	0.30	0.768
Central	Cmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.25	0.12	-2.08	0.038	-0.28	0.13	-2.17	0.030
Central	Cmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.03	0.15	0.17	0.869	0.02	0.14	0.17	0.869
Central	Cmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.25	0.12	-2.08	0.038	-0.28	0.13	-2.16	0.031
Central	Cmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.15	0.16	0.873	0.00	0.14	0.03	0.976
Central	Cmic	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	Cmic	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	Cmic	pH	Cmic	~	pH_historic	c	0.00	0.14	-0.02	0.985	0.00	0.13	-0.02	0.985
Central	Cmic	pH	Cmic	~	pH_change	d	-0.15	0.15	-1.05	0.296	-0.14	0.13	-1.06	0.291
Central	Cmic	pH	Cmic	~	LUI_historic	e	-0.26	0.12	-2.23	0.026	-0.30	0.13	-2.33	0.020
Central	Cmic	pH	Cmic	~	LUI_change	f	0.00	0.15	0.02	0.983	0.00	0.14	0.02	0.983
Central	Cmic	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	Cmic	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	Cmic	pH	Cmic	~~	Cmic		0.05	0.01	5.00	0.000	0.89	0.08	10.85	0.000
Central	Cmic	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.02	0.985	0.00	0.01	0.02	0.985
Central	Cmic	pH	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.03	0.75	0.455	0.02	0.03	0.75	0.453
Central	Cmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.26	0.12	-2.23	0.026	-0.30	0.13	-2.33	0.020
Central	Cmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.03	0.15	0.18	0.860	0.02	0.14	0.18	0.860
Central	Cmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.26	0.12	-2.23	0.026	-0.30	0.13	-2.32	0.020
Central	Cmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.03	0.15	0.17	0.864	0.01	0.14	0.03	0.972
Central	Nmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	Nmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	Nmic	CWM_leaf_P	Nmic	~	CWM_leafP_historic	c	-0.17	0.15	-1.12	0.264	-0.18	0.16	-1.13	0.259
Central	Nmic	CWM_leaf_P	Nmic	~	CWM_leafP_change	d	-0.03	0.17	-0.17	0.862	-0.02	0.13	-0.17	0.862
Central	Nmic	CWM_leaf_P	Nmic	~	LUI_historic	e	-0.25	0.13	-2.00	0.045	-0.32	0.16	-2.06	0.039
Central	Nmic	CWM_leaf_P	Nmic	~	LUI_change	f	-0.08	0.13	-0.64	0.524	-0.08	0.13	-0.64	0.523
Central	Nmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Nmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	Nmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	Nmic	CWM_leaf_P	Nmic	~~	Nmic		0.03	0.01	5.00	0.000	0.78	0.10	7.49	0.000
Central	Nmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.09	0.08	-1.10	0.272	-0.12	0.10	-1.11	0.267
Central	Nmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.16	0.871	0.00	0.01	0.16	0.871
Central	Nmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.34	0.10	-3.47	0.001	-0.44	0.11	-3.86	0.000
Central	Nmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.08	0.13	-0.63	0.530	-0.08	0.13	-0.63	0.529
Central	Nmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.34	0.10	-3.48	0.001	-0.44	0.11	-3.91	0.000
Central	Nmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.08	0.13	-0.64	0.524	-0.11	0.14	-0.77	0.442

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
Central	Nmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	Nmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	Nmic	CWM_MycInt	Nmic	~	CWM_MycInt_historic	c	0.14	0.11	1.25	0.211	0.16	0.13	1.26	0.207
Central	Nmic	CWM_MycInt	Nmic	~	CWM_MycInt_change	d	-0.09	0.14	-0.67	0.502	-0.08	0.13	-0.67	0.501
Central	Nmic	CWM_MycInt	Nmic	~	LUI_historic	e	-0.30	0.10	-3.09	0.002	-0.39	0.12	-3.33	0.001
Central	Nmic	CWM_MycInt	Nmic	~	LUI_change	f	-0.10	0.12	-0.77	0.444	-0.10	0.13	-0.77	0.442
Central	Nmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Nmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	Nmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	Nmic	CWM_MycInt	Nmic	~~	Nmic		0.03	0.01	5.00	0.000	0.79	0.10	7.66	0.000
Central	Nmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.02	-0.72	0.473	-0.02	0.03	-0.73	0.468
Central	Nmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.27	0.787	0.00	0.01	-0.27	0.787
Central	Nmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.31	0.10	-3.21	0.001	-0.41	0.12	-3.52	0.000
Central	Nmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.10	0.13	-0.79	0.429	-0.10	0.13	-0.79	0.428
Central	Nmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.31	0.10	-3.22	0.001	-0.42	0.12	-3.57	0.000
Central	Nmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.13	-0.80	0.425	-0.13	0.14	-0.92	0.360
Central	Nmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	Nmic	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	Nmic	Plant_biomass	Nmic	~	Plant_biomass	c	0.10	0.12	0.81	0.417	0.10	0.13	0.82	0.415
Central	Nmic	Plant_biomass	Nmic	~	LUI_historic	e	-0.34	0.10	-3.52	0.000	-0.44	0.11	-3.91	0.000
Central	Nmic	Plant_biomass	Nmic	~	LUI_change	f	-0.10	0.13	-0.76	0.445	-0.10	0.13	-0.77	0.444
Central	Nmic	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Nmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	Nmic	Plant_biomass	Nmic	~~	Nmic		0.03	0.01	5.00	0.000	0.79	0.10	7.64	0.000
Central	Nmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.22	0.827	0.00	0.02	0.22	0.827
Central	Nmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.59	0.553	0.01	0.02	0.59	0.553
Central	Nmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.34	0.10	-3.47	0.001	-0.44	0.11	-3.85	0.000
Central	Nmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.08	0.13	-0.67	0.506	-0.08	0.13	-0.67	0.505
Central	Nmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.34	0.10	-3.47	0.001	-0.44	0.11	-3.91	0.000
Central	Nmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.13	-0.67	0.501	-0.11	0.14	-0.80	0.422
Central	Nmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	Nmic	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	Nmic	Lignin_content	Nmic	~	Lignin_content	c	0.12	0.11	1.07	0.283	0.14	0.13	1.08	0.280
Central	Nmic	Lignin_content	Nmic	~	LUI_historic	e	-0.35	0.10	-3.59	0.000	-0.45	0.11	-3.99	0.000
Central	Nmic	Lignin_content	Nmic	~	LUI_change	f	-0.09	0.13	-0.74	0.459	-0.09	0.13	-0.74	0.457
Central	Nmic	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Nmic	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	Nmic	Lignin_content	Nmic	~~	Nmic		0.03	0.01	5.00	0.000	0.78	0.10	7.50	0.000
Central	Nmic	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.52	0.600	0.01	0.02	0.52	0.601
Central	Nmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.43	0.670	0.01	0.02	0.43	0.670
Central	Nmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.34	0.10	-3.47	0.001	-0.44	0.11	-3.85	0.000
Central	Nmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.08	0.13	-0.67	0.506	-0.08	0.13	-0.67	0.505
Central	Nmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.34	0.10	-3.47	0.001	-0.44	0.11	-3.91	0.000
Central	Nmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.13	-0.67	0.501	-0.11	0.14	-0.80	0.422
Central	Nmic	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	Nmic	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	Nmic	pH	Nmic	~	pH_historic	c	0.07	0.12	0.58	0.562	0.07	0.13	0.58	0.561
Central	Nmic	pH	Nmic	~	pH_change	d	0.06	0.12	0.48	0.633	0.06	0.13	0.48	0.633
Central	Nmic	pH	Nmic	~	LUI_historic	e	-0.33	0.10	-3.38	0.001	-0.43	0.11	-3.73	0.000
Central	Nmic	pH	Nmic	~	LUI_change	f	-0.09	0.13	-0.72	0.474	-0.09	0.13	-0.72	0.472
Central	Nmic	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Nmic	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	Nmic	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	Nmic	pH	Nmic	~~	Nmic		0.03	0.01	5.00	0.000	0.79	0.10	7.74	0.000
Central	Nmic	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Nmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.28	0.778	0.00	0.01	-0.28	0.778
Central	Nmic	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.02	-0.44	0.663	-0.01	0.02	-0.44	0.663
Central	Nmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.33	0.10	-3.40	0.001	-0.43	0.11	-3.76	0.000
Central	Nmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.10	0.13	-0.80	0.427	-0.10	0.13	-0.80	0.425
Central	Nmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.33	0.10	-3.41	0.001	-0.44	0.11	-3.82	0.000
Central	Nmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.10	0.13	-0.80	0.422	-0.13	0.14	-0.92	0.357

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
Central	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	CWM_leafP_historic	c	0.02	0.18	0.11	0.915	0.02	0.17	0.11	0.915
Central	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	CWM_leafP_change	d	0.07	0.21	0.36	0.722	0.05	0.13	0.36	0.721
Central	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	LUI_historic	e	0.27	0.15	1.78	0.076	0.31	0.17	1.83	0.067
Central	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	LUI_change	f	-0.07	0.15	-0.48	0.633	-0.06	0.13	-0.48	0.633
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	5.00	0.000	0.89	0.08	10.83	0.000
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.10	0.11	0.915	0.01	0.11	0.11	0.915
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.28	0.779	0.00	0.01	-0.28	0.778
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.28	0.12	2.39	0.017	0.32	0.13	2.52	0.012
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.08	0.15	-0.50	0.617	-0.07	0.13	-0.50	0.616
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.28	0.12	2.39	0.017	0.32	0.13	2.49	0.013
Central	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.08	0.15	-0.49	0.621	-0.05	0.14	-0.33	0.741
Central	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	CWM_MycInt_historic	c	0.01	0.13	0.10	0.921	0.01	0.14	0.10	0.921
Central	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	CWM_MycInt_change	d	0.22	0.17	1.32	0.187	0.18	0.13	1.34	0.180
Central	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	LUI_historic	e	0.22	0.12	1.89	0.059	0.26	0.13	1.95	0.052
Central	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	LUI_change	f	-0.08	0.15	-0.53	0.595	-0.07	0.13	-0.53	0.594
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	5.00	0.000	0.90	0.08	11.40	0.000
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.10	0.922	0.00	0.02	-0.10	0.922
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.03	0.29	0.773	0.01	0.03	0.29	0.773
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.22	0.12	1.89	0.059	0.25	0.13	1.95	0.051
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.07	0.15	-0.47	0.639	-0.06	0.14	-0.47	0.638
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.22	0.12	1.89	0.059	0.25	0.13	1.92	0.056
Central	Cmic:Nmic ratio	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.07	0.15	-0.46	0.642	-0.05	0.14	-0.34	0.734
Central	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	Plant_biomass	c	-0.16	0.14	-1.14	0.254	-0.15	0.13	-1.15	0.249
Central	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	LUI_historic	e	0.29	0.12	2.45	0.014	0.32	0.13	2.58	0.010
Central	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	LUI_change	f	-0.06	0.15	-0.36	0.719	-0.05	0.13	-0.36	0.719
Central	Cmic:Nmic ratio	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	5.00	0.000	0.87	0.09	9.94	0.000
Central	Cmic:Nmic ratio	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.22	0.824	-0.01	0.02	-0.22	0.824
Central	Cmic:Nmic ratio	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.02	0.03	-0.69	0.489	-0.02	0.03	-0.69	0.488
Central	Cmic:Nmic ratio	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.28	0.12	2.38	0.017	0.32	0.13	2.51	0.012
Central	Cmic:Nmic ratio	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.08	0.15	-0.50	0.620	-0.07	0.13	-0.50	0.619
Central	Cmic:Nmic ratio	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.28	0.12	2.38	0.017	0.32	0.13	2.47	0.013
Central	Cmic:Nmic ratio	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.08	0.15	-0.49	0.624	-0.05	0.14	-0.33	0.744
Central	Cmic:Nmic ratio	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	Cmic:Nmic ratio	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	Lignin_content	c	-0.08	0.14	-0.57	0.570	-0.08	0.13	-0.57	0.569
Central	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	LUI_historic	e	0.29	0.12	2.43	0.015	0.33	0.13	2.56	0.010
Central	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	LUI_change	f	-0.07	0.15	-0.46	0.646	-0.06	0.13	-0.46	0.646
Central	Cmic:Nmic ratio	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic:Nmic ratio	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.05	0.01	5.00	0.000	0.89	0.08	10.69	0.000
Central	Cmic:Nmic ratio	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.01	-0.41	0.680	-0.01	0.02	-0.41	0.680
Central	Cmic:Nmic ratio	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.02	-0.36	0.719	-0.01	0.01	-0.36	0.719
Central	Cmic:Nmic ratio	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.28	0.12	2.38	0.017	0.32	0.13	2.51	0.012
Central	Cmic:Nmic ratio	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.08	0.15	-0.50	0.620	-0.07	0.13	-0.50	0.619
Central	Cmic:Nmic ratio	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.28	0.12	2.38	0.017	0.32	0.13	2.47	0.013
Central	Cmic:Nmic ratio	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.08	0.15	-0.49	0.624	-0.05	0.14	-0.33	0.744

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
Central	Cmic:Nmic ratio	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	Cmic:Nmic ratio	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	pH_historic	c	-0.50	0.14	-3.68	0.000	-0.42	0.11	-3.97	0.000
Central	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	pH_change	d	-0.37	0.14	-2.74	0.006	-0.32	0.11	-2.83	0.005
Central	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	LUI_historic	e	0.22	0.11	2.05	0.041	0.24	0.11	2.08	0.037
Central	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	LUI_change	f	-0.02	0.14	-0.13	0.897	-0.02	0.12	-0.13	0.897
Central	Cmic:Nmic ratio	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	Cmic:Nmic ratio	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	Cmic:Nmic ratio	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.04	0.01	5.00	0.000	0.66	0.11	6.26	0.000
Central	Cmic:Nmic ratio	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	Cmic:Nmic ratio	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.06	0.32	0.748	0.02	0.06	0.32	0.747
Central	Cmic:Nmic ratio	pH	LUI_change_in	:=	b*d	LUI_change_in	0.06	0.06	1.00	0.320	0.05	0.05	1.00	0.317
Central	Cmic:Nmic ratio	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.24	0.12	1.97	0.049	0.26	0.13	2.03	0.043
Central	Cmic:Nmic ratio	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.04	0.15	0.26	0.793	0.03	0.12	0.26	0.793
Central	Cmic:Nmic ratio	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.24	0.12	1.97	0.049	0.26	0.13	2.05	0.041
Central	Cmic:Nmic ratio	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.04	0.15	0.27	0.789	0.05	0.13	0.38	0.704
Central	Pmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.54	0.09	5.79	0.000	0.65	0.09	7.65	0.000
Central	Pmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.07	0.11	-0.59	0.557	-0.09	0.15	-0.59	0.555
Central	Pmic	CWM_leaf_P	Pmic	~	CWM_leafP_historic	c	0.34	0.19	1.78	0.075	0.33	0.18	1.84	0.066
Central	Pmic	CWM_leaf_P	Pmic	~	CWM_leafP_change	d	0.21	0.21	0.98	0.326	0.14	0.14	0.99	0.322
Central	Pmic	CWM_leaf_P	Pmic	~	LUI_historic	e	-0.10	0.16	-0.62	0.536	-0.12	0.19	-0.62	0.534
Central	Pmic	CWM_leaf_P	Pmic	~	LUI_change	f	0.08	0.16	0.52	0.605	0.07	0.14	0.52	0.604
Central	Pmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.48	0.629	0.07	0.15	0.49	0.626
Central	Pmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.74	0.000	0.57	0.11	5.13	0.000
Central	Pmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.01	4.74	0.000	0.99	0.03	38.44	0.000
Central	Pmic	CWM_leaf_P	Pmic	~~	Pmic		0.05	0.01	4.74	0.000	0.90	0.08	10.81	0.000
Central	Pmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.18	0.11	1.70	0.089	0.22	0.12	1.75	0.080
Central	Pmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.03	-0.50	0.614	-0.01	0.02	-0.51	0.614
Central	Pmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.09	0.12	0.69	0.489	0.10	0.15	0.70	0.487
Central	Pmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.07	0.16	0.43	0.668	0.06	0.14	0.43	0.668
Central	Pmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.09	0.12	0.69	0.487	0.11	0.15	0.73	0.467
Central	Pmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.07	0.16	0.43	0.667	0.07	0.14	0.48	0.632
Central	Pmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.12	0.14	-0.92	0.359	-0.14	0.15	-0.93	0.354
Central	Pmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.02	0.14	0.17	0.868	0.03	0.15	0.17	0.868
Central	Pmic	CWM_MycInt	Pmic	~	CWM_MycInt_historic	c	0.01	0.14	0.05	0.957	0.01	0.15	0.05	0.957
Central	Pmic	CWM_MycInt	Pmic	~	CWM_MycInt_change	d	0.10	0.17	0.58	0.564	0.09	0.15	0.58	0.563
Central	Pmic	CWM_MycInt	Pmic	~	LUI_historic	e	0.05	0.12	0.44	0.661	0.07	0.15	0.44	0.660
Central	Pmic	CWM_MycInt	Pmic	~	LUI_change	f	0.06	0.16	0.37	0.711	0.06	0.15	0.37	0.711
Central	Pmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.48	0.629	0.07	0.15	0.49	0.626
Central	Pmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.06	0.01	4.74	0.000	0.98	0.04	24.75	0.000
Central	Pmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.04	0.01	4.74	0.000	1.00	0.01	135.81	0.000
Central	Pmic	CWM_MycInt	Pmic	~~	Pmic		0.05	0.01	4.74	0.000	0.99	0.04	27.13	0.000
Central	Pmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.05	0.957	0.00	0.02	-0.05	0.957
Central	Pmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.16	0.873	0.00	0.01	0.16	0.873
Central	Pmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.12	0.44	0.663	0.07	0.15	0.44	0.663
Central	Pmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.06	0.16	0.38	0.701	0.06	0.15	0.38	0.701
Central	Pmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.12	0.44	0.662	0.07	0.15	0.47	0.642
Central	Pmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.06	0.16	0.39	0.700	0.06	0.15	0.42	0.677
Central	Pmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.13	0.21	0.836	0.03	0.15	0.21	0.836
Central	Pmic	Plant_biomass	Plant_biomass	~	LUI_change	b	0.14	0.16	0.85	0.393	0.13	0.15	0.86	0.390
Central	Pmic	Plant_biomass	Pmic	~	Plant_biomass	c	-0.16	0.15	-1.07	0.284	-0.16	0.15	-1.09	0.278
Central	Pmic	Plant_biomass	Pmic	~	LUI_historic	e	0.09	0.12	0.72	0.472	0.11	0.15	0.72	0.469
Central	Pmic	Plant_biomass	Pmic	~	LUI_change	f	0.08	0.16	0.51	0.611	0.08	0.15	0.51	0.611
Central	Pmic	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.48	0.629	0.07	0.15	0.49	0.626
Central	Pmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.74	0.000	0.98	0.04	25.37	0.000
Central	Pmic	Plant_biomass	Pmic	~~	Pmic		0.05	0.01	4.74	0.000	0.96	0.06	17.09	0.000
Central	Pmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.20	0.839	-0.01	0.02	-0.20	0.839
Central	Pmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.02	0.03	-0.67	0.504	-0.02	0.03	-0.67	0.503
Central	Pmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.08	0.12	0.68	0.497	0.10	0.15	0.68	0.495
Central	Pmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.06	0.16	0.37	0.711	0.06	0.15	0.37	0.710
Central	Pmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.08	0.12	0.68	0.496	0.11	0.15	0.71	0.478
Central	Pmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.06	0.16	0.37	0.709	0.06	0.15	0.42	0.675

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
Central	Pmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.10	0.13	0.75	0.455	0.11	0.15	0.75	0.452
Central	Pmic	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.17	0.38	0.703	0.06	0.15	0.38	0.703
Central	Pmic	Lignin_content	Pmic	~	Lignin_content	c	0.00	0.14	0.02	0.984	0.00	0.15	0.02	0.984
Central	Pmic	Lignin_content	Pmic	~	LUI_historic	e	0.08	0.12	0.67	0.501	0.10	0.15	0.68	0.499
Central	Pmic	Lignin_content	Pmic	~	LUI_change	f	0.06	0.16	0.37	0.712	0.06	0.15	0.37	0.711
Central	Pmic	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.48	0.629	0.07	0.15	0.49	0.626
Central	Pmic	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.74	0.000	0.98	0.04	26.22	0.000
Central	Pmic	Lignin_content	Pmic	~~	Pmic		0.05	0.01	4.74	0.000	0.99	0.04	28.36	0.000
Central	Pmic	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.02	0.984	0.00	0.02	0.02	0.984
Central	Pmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.02	0.984	0.00	0.01	0.02	0.984
Central	Pmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.08	0.12	0.68	0.497	0.10	0.15	0.68	0.495
Central	Pmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.06	0.16	0.37	0.711	0.06	0.15	0.37	0.710
Central	Pmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.08	0.12	0.68	0.496	0.11	0.15	0.71	0.478
Central	Pmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.06	0.16	0.37	0.709	0.06	0.15	0.42	0.675
Central	Pmic	pH	pH_historic	~	LUI_historic	a	-0.02	0.12	-0.16	0.875	-0.02	0.15	-0.16	0.875
Central	Pmic	pH	pH_change	~	LUI_change	b	-0.16	0.16	-1.01	0.314	-0.15	0.15	-1.02	0.309
Central	Pmic	pH	Pmic	~	pH_historic	c	0.22	0.15	1.46	0.143	0.21	0.14	1.50	0.135
Central	Pmic	pH	Pmic	~	pH_change	d	0.16	0.15	1.04	0.297	0.15	0.14	1.05	0.292
Central	Pmic	pH	Pmic	~	LUI_historic	e	0.11	0.12	0.92	0.357	0.13	0.14	0.93	0.353
Central	Pmic	pH	Pmic	~	LUI_change	f	0.04	0.16	0.23	0.820	0.03	0.15	0.23	0.820
Central	Pmic	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.48	0.629	0.07	0.15	0.49	0.626
Central	Pmic	pH	pH_historic	~~	pH_historic		0.05	0.01	4.74	0.000	1.00	0.01	143.35	0.000
Central	Pmic	pH	pH_change	~~	pH_change		0.04	0.01	4.74	0.000	0.98	0.04	22.61	0.000
Central	Pmic	pH	Pmic	~~	Pmic		0.05	0.01	4.74	0.000	0.92	0.08	11.79	0.000
Central	Pmic	pH	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	pH	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	Pmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.03	-0.16	0.876	-0.01	0.03	-0.16	0.876
Central	Pmic	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.03	0.03	-0.72	0.469	-0.02	0.03	-0.73	0.467
Central	Pmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.11	0.12	0.87	0.386	0.13	0.15	0.87	0.382
Central	Pmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.01	0.16	0.07	0.941	0.01	0.15	0.07	0.941
Central	Pmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.11	0.12	0.87	0.385	0.13	0.15	0.88	0.378
Central	Pmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.01	0.16	0.08	0.939	0.02	0.15	0.14	0.892
Central	beta-glucosidase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	beta-glucosidase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	beta-glucosidase	CWM_leaf_P	Glucosidase	~	CWM_leafP_historic	c	-0.16	0.11	-1.47	0.141	-0.21	0.14	-1.48	0.139
Central	beta-glucosidase	CWM_leaf_P	Glucosidase	~	CWM_leafP_change	d	-0.59	0.12	-4.76	0.000	-0.53	0.10	-5.45	0.000
Central	beta-glucosidase	CWM_leaf_P	Glucosidase	~	LUI_historic	e	-0.08	0.09	-0.84	0.401	-0.12	0.14	-0.84	0.400
Central	beta-glucosidase	CWM_leaf_P	Glucosidase	~	LUI_change	f	0.13	0.09	1.43	0.153	0.16	0.11	1.44	0.151
Central	beta-glucosidase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	beta-glucosidase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	beta-glucosidase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	beta-glucosidase	CWM_leaf_P	Glucosidase	~~	Glucosidase		0.02	0.00	5.00	0.000	0.61	0.10	5.82	0.000
Central	beta-glucosidase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.09	0.06	-1.43	0.154	-0.13	0.09	-1.44	0.150
Central	beta-glucosidase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.03	0.06	0.46	0.649	0.03	0.07	0.46	0.647
Central	beta-glucosidase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.16	0.07	-2.25	0.024	-0.25	0.11	-2.29	0.022
Central	beta-glucosidase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.16	0.11	1.44	0.149	0.19	0.13	1.47	0.143
Central	beta-glucosidase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.16	0.07	-2.25	0.025	-0.24	0.11	-2.12	0.034
Central	beta-glucosidase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.16	0.11	1.44	0.150	0.18	0.14	1.30	0.195
Central	beta-glucosidase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	beta-glucosidase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	beta-glucosidase	CWM_MycInt	Glucosidase	~	CWM_MycInt_historic	c	-0.17	0.09	-1.84	0.065	-0.24	0.13	-1.89	0.059
Central	beta-glucosidase	CWM_MycInt	Glucosidase	~	CWM_MycInt_change	d	-0.08	0.12	-0.67	0.503	-0.09	0.13	-0.67	0.502
Central	beta-glucosidase	CWM_MycInt	Glucosidase	~	LUI_historic	e	-0.15	0.08	-1.86	0.063	-0.25	0.13	-1.91	0.056
Central	beta-glucosidase	CWM_MycInt	Glucosidase	~	LUI_change	f	0.17	0.11	1.61	0.108	0.21	0.13	1.64	0.102
Central	beta-glucosidase	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	beta-glucosidase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	beta-glucosidase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	beta-glucosidase	CWM_MycInt	Glucosidase	~~	Glucosidase		0.02	0.00	5.00	0.000	0.85	0.09	9.27	0.000
Central	beta-glucosidase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.02	0.79	0.428	0.03	0.04	0.79	0.428
Central	beta-glucosidase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.27	0.787	0.00	0.01	-0.27	0.787
Central	beta-glucosidase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.14	0.09	-1.59	0.111	-0.22	0.13	-1.63	0.103
Central	beta-glucosidase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.17	0.11	1.57	0.116	0.21	0.13	1.60	0.109
Central	beta-glucosidase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.14	0.09	-1.59	0.113	-0.20	0.14	-1.50	0.135
Central	beta-glucosidase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.17	0.11	1.57	0.117	0.19	0.13	1.46	0.145

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
Central	beta-glucosidase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	beta-glucosidase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	beta-glucosidase	Plant_biomass	Glucosidase	~	Plant_biomass	c	0.21	0.10	2.09	0.037	0.27	0.13	2.16	0.031
Central	beta-glucosidase	Plant_biomass	Glucosidase	~	LUI_historic	e	-0.16	0.08	-1.98	0.047	-0.26	0.13	-2.04	0.041
Central	beta-glucosidase	Plant_biomass	Glucosidase	~	LUI_change	f	0.13	0.11	1.20	0.232	0.16	0.13	1.21	0.227
Central	beta-glucosidase	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	beta-glucosidase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	beta-glucosidase	Plant_biomass	Glucosidase	~~	Glucosidase		0.02	0.00	5.00	0.000	0.84	0.10	8.72	0.000
Central	beta-glucosidase	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.23	0.822	0.01	0.04	0.23	0.822
Central	beta-glucosidase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.03	0.03	0.80	0.423	0.03	0.04	0.81	0.418
Central	beta-glucosidase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.16	0.09	-1.84	0.066	-0.25	0.13	-1.90	0.058
Central	beta-glucosidase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.15	0.11	1.40	0.161	0.19	0.13	1.43	0.154
Central	beta-glucosidase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.16	0.09	-1.83	0.067	-0.24	0.13	-1.77	0.077
Central	beta-glucosidase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.15	0.11	1.40	0.162	0.17	0.14	1.27	0.206
Central	beta-glucosidase	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	beta-glucosidase	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	beta-glucosidase	Lignin_content	Glucosidase	~	Lignin_content	c	0.10	0.10	1.04	0.300	0.14	0.13	1.05	0.296
Central	beta-glucosidase	Lignin_content	Glucosidase	~	LUI_historic	e	-0.16	0.09	-1.94	0.052	-0.26	0.13	-2.00	0.045
Central	beta-glucosidase	Lignin_content	Glucosidase	~	LUI_change	f	0.15	0.11	1.35	0.178	0.18	0.13	1.37	0.172
Central	beta-glucosidase	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	beta-glucosidase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	beta-glucosidase	Lignin_content	Glucosidase	~~	Glucosidase		0.02	0.01	5.00	0.000	0.89	0.08	10.63	0.000
Central	beta-glucosidase	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.01	0.52	0.603	0.01	0.02	0.52	0.603
Central	beta-glucosidase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.42	0.672	0.01	0.02	0.43	0.671
Central	beta-glucosidase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.16	0.09	-1.84	0.066	-0.25	0.13	-1.90	0.058
Central	beta-glucosidase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.15	0.11	1.40	0.161	0.19	0.13	1.43	0.154
Central	beta-glucosidase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.16	0.09	-1.83	0.067	-0.24	0.13	-1.77	0.077
Central	beta-glucosidase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.15	0.11	1.40	0.162	0.17	0.14	1.27	0.206
Central	beta-glucosidase	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	beta-glucosidase	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	beta-glucosidase	pH	Glucosidase	~	pH_historic	c	0.09	0.10	0.83	0.409	0.11	0.13	0.83	0.406
Central	beta-glucosidase	pH	Glucosidase	~	pH_change	d	-0.04	0.11	-0.41	0.680	-0.06	0.14	-0.41	0.679
Central	beta-glucosidase	pH	Glucosidase	~	LUI_historic	e	-0.16	0.08	-1.86	0.063	-0.25	0.13	-1.92	0.055
Central	beta-glucosidase	pH	Glucosidase	~	LUI_change	f	0.13	0.11	1.17	0.244	0.16	0.13	1.18	0.238
Central	beta-glucosidase	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	beta-glucosidase	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	beta-glucosidase	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	beta-glucosidase	pH	Glucosidase	~~	Glucosidase		0.02	0.01	5.00	0.000	0.90	0.08	11.07	0.000
Central	beta-glucosidase	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	beta-glucosidase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.30	0.764	-0.01	0.02	-0.30	0.764
Central	beta-glucosidase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.02	0.39	0.700	0.01	0.02	0.39	0.700
Central	beta-glucosidase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.16	0.09	-1.89	0.059	-0.26	0.13	-1.95	0.051
Central	beta-glucosidase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.14	0.11	1.24	0.215	0.17	0.13	1.26	0.209
Central	beta-glucosidase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.16	0.09	-1.88	0.060	-0.24	0.13	-1.84	0.066
Central	beta-glucosidase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.14	0.11	1.24	0.217	0.15	0.14	1.10	0.274
Central	beta-xylosidase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.47	0.09	5.05	0.000	0.59	0.09	6.24	0.000
Central	beta-xylosidase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.04	0.11	-0.35	0.724	-0.05	0.14	-0.35	0.724
Central	beta-xylosidase	CWM_leaf_P	Xylosidase	~	CWM_leafP_historic	c	0.04	0.13	0.29	0.773	0.05	0.16	0.29	0.773
Central	beta-xylosidase	CWM_leaf_P	Xylosidase	~	CWM_leafP_change	d	-0.41	0.13	-3.08	0.002	-0.39	0.12	-3.31	0.001
Central	beta-xylosidase	CWM_leaf_P	Xylosidase	~	LUI_historic	e	-0.15	0.10	-1.45	0.147	-0.23	0.15	-1.47	0.142
Central	beta-xylosidase	CWM_leaf_P	Xylosidase	~	LUI_change	f	0.16	0.10	1.56	0.119	0.20	0.12	1.58	0.113
Central	beta-xylosidase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.06	0.949	0.01	0.14	0.06	0.949
Central	beta-xylosidase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.90	0.000	0.65	0.11	5.89	0.000
Central	beta-xylosidase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.01	4.90	0.000	1.00	0.02	68.09	0.000
Central	beta-xylosidase	CWM_leaf_P	Xylosidase	~~	Xylosidase		0.02	0.00	4.90	0.000	0.76	0.11	7.20	0.000
Central	beta-xylosidase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.06	0.29	0.774	0.03	0.09	0.29	0.774
Central	beta-xylosidase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.05	0.35	0.726	0.02	0.06	0.35	0.725
Central	beta-xylosidase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.08	-1.58	0.114	-0.20	0.12	-1.61	0.108
Central	beta-xylosidase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.17	0.11	1.57	0.116	0.22	0.14	1.61	0.108
Central	beta-xylosidase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.13	0.08	-1.58	0.114	-0.20	0.13	-1.55	0.122
Central	beta-xylosidase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.17	0.11	1.57	0.116	0.22	0.14	1.56	0.118

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
Central	beta-xylosidase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.07	0.13	-0.53	0.596	-0.08	0.14	-0.53	0.595
Central	beta-xylosidase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.01	0.13	0.08	0.935	0.01	0.14	0.08	0.935
Central	beta-xylosidase	CWM_MycInt	Xylosidase	~	CWM_MycInt_historic	c	-0.12	0.10	-1.23	0.218	-0.17	0.13	-1.25	0.213
Central	beta-xylosidase	CWM_MycInt	Xylosidase	~	CWM_MycInt_change	d	0.08	0.12	0.62	0.533	0.08	0.13	0.63	0.532
Central	beta-xylosidase	CWM_MycInt	Xylosidase	~	LUI_historic	e	-0.16	0.09	-1.78	0.076	-0.24	0.13	-1.82	0.068
Central	beta-xylosidase	CWM_MycInt	Xylosidase	~	LUI_change	f	0.19	0.11	1.72	0.085	0.23	0.13	1.76	0.078
Central	beta-xylosidase	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.06	0.949	0.01	0.14	0.06	0.949
Central	beta-xylosidase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.90	0.000	0.99	0.02	45.45	0.000
Central	beta-xylosidase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.90	0.000	1.00	0.00	295.85	0.000
Central	beta-xylosidase	CWM_MycInt	Xylosidase	~~	Xylosidase		0.02	0.01	4.90	0.000	0.86	0.09	9.40	0.000
Central	beta-xylosidase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.49	0.627	0.01	0.03	0.49	0.627
Central	beta-xylosidase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.08	0.936	0.00	0.01	0.08	0.936
Central	beta-xylosidase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.15	0.09	-1.66	0.097	-0.23	0.13	-1.70	0.089
Central	beta-xylosidase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.19	0.11	1.72	0.085	0.23	0.13	1.77	0.078
Central	beta-xylosidase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.15	0.09	-1.66	0.097	-0.22	0.14	-1.64	0.101
Central	beta-xylosidase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.19	0.11	1.72	0.085	0.23	0.14	1.70	0.089
Central	beta-xylosidase	Plant_biomass	Plant_biomass	~	LUI_historic	a	-0.01	0.12	-0.09	0.925	-0.01	0.14	-0.09	0.925
Central	beta-xylosidase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.10	0.16	0.65	0.518	0.09	0.14	0.65	0.516
Central	beta-xylosidase	Plant_biomass	Xylosidase	~	Plant_biomass	c	0.25	0.10	2.53	0.011	0.33	0.12	2.67	0.008
Central	beta-xylosidase	Plant_biomass	Xylosidase	~	LUI_historic	e	-0.13	0.08	-1.49	0.137	-0.19	0.13	-1.51	0.131
Central	beta-xylosidase	Plant_biomass	Xylosidase	~	LUI_change	f	0.15	0.11	1.42	0.156	0.19	0.13	1.44	0.150
Central	beta-xylosidase	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.06	0.949	0.01	0.14	0.06	0.949
Central	beta-xylosidase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.90	0.000	0.99	0.03	36.93	0.000
Central	beta-xylosidase	Plant_biomass	Xylosidase	~~	Xylosidase		0.02	0.00	4.90	0.000	0.81	0.10	7.90	0.000
Central	beta-xylosidase	Plant_biomass	LUI_historic	~~	LUI_historic		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.03	-0.09	0.925	0.00	0.05	-0.09	0.925
Central	beta-xylosidase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.03	0.04	0.63	0.531	0.03	0.05	0.63	0.527
Central	beta-xylosidase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.09	-1.43	0.153	-0.20	0.14	-1.46	0.145
Central	beta-xylosidase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.17	0.11	1.56	0.119	0.22	0.14	1.60	0.110
Central	beta-xylosidase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.13	0.09	-1.43	0.153	-0.20	0.14	-1.41	0.159
Central	beta-xylosidase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.17	0.11	1.56	0.119	0.21	0.14	1.55	0.121
Central	beta-xylosidase	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.13	0.53	0.595	0.08	0.14	0.53	0.594
Central	beta-xylosidase	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.45	0.656	0.06	0.14	0.45	0.655
Central	beta-xylosidase	Lignin_content	Xylosidase	~	Lignin_content	c	0.23	0.09	2.55	0.011	0.33	0.12	2.68	0.007
Central	beta-xylosidase	Lignin_content	Xylosidase	~	LUI_historic	e	-0.14	0.08	-1.72	0.086	-0.22	0.13	-1.75	0.080
Central	beta-xylosidase	Lignin_content	Xylosidase	~	LUI_change	f	0.16	0.11	1.50	0.135	0.19	0.13	1.52	0.129
Central	beta-xylosidase	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.06	0.949	0.01	0.14	0.06	0.949
Central	beta-xylosidase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.90	0.000	0.99	0.03	34.64	0.000
Central	beta-xylosidase	Lignin_content	Xylosidase	~~	Xylosidase		0.02	0.00	4.90	0.000	0.81	0.10	7.87	0.000
Central	beta-xylosidase	Lignin_content	LUI_historic	~~	LUI_historic		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.03	0.52	0.603	0.03	0.05	0.52	0.604
Central	beta-xylosidase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.04	0.44	0.661	0.02	0.05	0.44	0.659
Central	beta-xylosidase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.09	-1.43	0.153	-0.20	0.14	-1.46	0.145
Central	beta-xylosidase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.17	0.11	1.56	0.119	0.22	0.14	1.60	0.110
Central	beta-xylosidase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.13	0.09	-1.43	0.153	-0.20	0.14	-1.41	0.159
Central	beta-xylosidase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.17	0.11	1.56	0.119	0.21	0.14	1.55	0.121
Central	beta-xylosidase	pH	pH_historic	~	LUI_historic	a	-0.01	0.12	-0.11	0.911	-0.02	0.14	-0.11	0.911
Central	beta-xylosidase	pH	pH_change	~	LUI_change	b	-0.15	0.15	-0.99	0.321	-0.14	0.14	-1.00	0.316
Central	beta-xylosidase	pH	Xylosidase	~	pH_historic	c	-0.03	0.10	-0.33	0.742	-0.04	0.13	-0.33	0.742
Central	beta-xylosidase	pH	Xylosidase	~	pH_change	d	-0.22	0.10	-2.12	0.034	-0.28	0.13	-2.20	0.028
Central	beta-xylosidase	pH	Xylosidase	~	LUI_historic	e	-0.15	0.09	-1.75	0.080	-0.23	0.13	-1.79	0.074
Central	beta-xylosidase	pH	Xylosidase	~	LUI_change	f	0.15	0.11	1.38	0.167	0.18	0.13	1.40	0.161
Central	beta-xylosidase	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.06	0.949	0.01	0.14	0.06	0.949
Central	beta-xylosidase	pH	pH_historic	~~	pH_historic		0.05	0.01	4.90	0.000	1.00	0.01	215.93	0.000
Central	beta-xylosidase	pH	pH_change	~~	pH_change		0.04	0.01	4.90	0.000	0.98	0.04	24.43	0.000
Central	beta-xylosidase	pH	Xylosidase	~~	Xylosidase		0.02	0.00	4.90	0.000	0.82	0.10	8.28	0.000
Central	beta-xylosidase	pH	LUI_historic	~~	LUI_historic		0.06	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	pH	LUI_change	~~	LUI_change		0.04	0.01	4.90	0.000	1.00	0.00	NA	NA
Central	beta-xylosidase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	0.11	0.916	0.00	0.01	0.11	0.916
Central	beta-xylosidase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.03	0.04	0.90	0.369	0.04	0.04	0.91	0.362
Central	beta-xylosidase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.15	0.09	-1.74	0.082	-0.23	0.13	-1.78	0.075
Central	beta-xylosidase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.18	0.11	1.63	0.104	0.22	0.13	1.67	0.096
Central	beta-xylosidase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.15	0.09	-1.74	0.082	-0.23	0.13	-1.72	0.086
Central	beta-xylosidase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.18	0.11	1.63	0.104	0.22	0.14	1.61	0.108

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
Central	chitinase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	chitinase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	chitinase	CWM_leaf_P	Chitinase	~	CWM_leafP_historic	c	-0.09	0.12	-0.76	0.449	-0.12	0.16	-0.76	0.447
Central	chitinase	CWM_leaf_P	Chitinase	~	CWM_leafP_change	d	-0.42	0.14	-3.00	0.003	-0.36	0.11	-3.18	0.001
Central	chitinase	CWM_leaf_P	Chitinase	~	LUI_historic	e	-0.19	0.10	-1.83	0.067	-0.29	0.15	-1.87	0.062
Central	chitinase	CWM_leaf_P	Chitinase	~	LUI_change	f	0.02	0.10	0.14	0.886	0.02	0.12	0.14	0.886
Central	chitinase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	chitinase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	chitinase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	chitinase	CWM_leaf_P	Chitinase	~~	Chitinase		0.02	0.00	5.00	0.000	0.73	0.10	7.04	0.000
Central	chitinase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.05	0.07	-0.75	0.453	-0.08	0.10	-0.75	0.451
Central	chitinase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.45	0.651	0.02	0.05	0.45	0.650
Central	chitinase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.24	0.08	-2.98	0.003	-0.36	0.12	-3.16	0.002
Central	chitinase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.04	0.11	0.31	0.756	0.04	0.13	0.31	0.756
Central	chitinase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.24	0.08	-2.98	0.003	-0.36	0.12	-3.13	0.002
Central	chitinase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.03	0.11	0.30	0.761	0.02	0.14	0.13	0.900
Central	chitinase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	chitinase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	chitinase	CWM_MycInt	Chitinase	~	CWM_MycInt_historic	c	-0.02	0.10	-0.23	0.815	-0.03	0.13	-0.23	0.815
Central	chitinase	CWM_MycInt	Chitinase	~	CWM_MycInt_change	d	-0.01	0.12	-0.06	0.953	-0.01	0.13	-0.06	0.953
Central	chitinase	CWM_MycInt	Chitinase	~	LUI_historic	e	-0.24	0.09	-2.70	0.007	-0.36	0.13	-2.89	0.004
Central	chitinase	CWM_MycInt	Chitinase	~	LUI_change	f	0.03	0.11	0.30	0.764	0.04	0.13	0.30	0.764
Central	chitinase	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	chitinase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	chitinase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	chitinase	CWM_MycInt	Chitinase	~~	Chitinase		0.03	0.01	5.00	0.000	0.87	0.09	9.90	0.000
Central	chitinase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.23	0.821	0.00	0.02	0.23	0.821
Central	chitinase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.06	0.954	0.00	0.01	-0.06	0.954
Central	chitinase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.23	0.09	-2.69	0.007	-0.36	0.12	-2.88	0.004
Central	chitinase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.03	0.11	0.30	0.766	0.04	0.13	0.30	0.766
Central	chitinase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.23	0.09	-2.69	0.007	-0.35	0.12	-2.86	0.004
Central	chitinase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.03	0.11	0.29	0.771	0.02	0.14	0.12	0.906
Central	chitinase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	chitinase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	chitinase	Plant_biomass	Chitinase	~	Plant_biomass	c	0.14	0.10	1.37	0.171	0.18	0.13	1.39	0.166
Central	chitinase	Plant_biomass	Chitinase	~	LUI_historic	e	-0.24	0.09	-2.80	0.005	-0.36	0.12	-3.00	0.003
Central	chitinase	Plant_biomass	Chitinase	~	LUI_change	f	0.01	0.11	0.12	0.907	0.02	0.13	0.12	0.907
Central	chitinase	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	chitinase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	chitinase	Plant_biomass	Chitinase	~~	Chitinase		0.02	0.01	5.00	0.000	0.84	0.10	8.85	0.000
Central	chitinase	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.22	0.823	0.01	0.03	0.22	0.823
Central	chitinase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.03	0.73	0.463	0.02	0.03	0.74	0.462
Central	chitinase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.24	0.09	-2.71	0.007	-0.36	0.12	-2.90	0.004
Central	chitinase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.03	0.11	0.28	0.779	0.04	0.13	0.28	0.779
Central	chitinase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.24	0.09	-2.71	0.007	-0.36	0.12	-2.88	0.004
Central	chitinase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.03	0.11	0.27	0.784	0.01	0.14	0.10	0.920
Central	chitinase	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	chitinase	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	chitinase	Lignin_content	Chitinase	~	Lignin_content	c	0.20	0.10	2.07	0.039	0.26	0.12	2.13	0.033
Central	chitinase	Lignin_content	Chitinase	~	LUI_historic	e	-0.25	0.08	-2.99	0.003	-0.38	0.12	-3.21	0.001
Central	chitinase	Lignin_content	Chitinase	~	LUI_change	f	0.02	0.11	0.16	0.876	0.02	0.13	0.16	0.876
Central	chitinase	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	chitinase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	chitinase	Lignin_content	Chitinase	~~	Chitinase		0.02	0.01	5.00	0.000	0.80	0.10	7.97	0.000
Central	chitinase	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.03	0.58	0.564	0.02	0.04	0.57	0.566
Central	chitinase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.03	0.45	0.650	0.02	0.04	0.45	0.650
Central	chitinase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.24	0.09	-2.71	0.007	-0.36	0.12	-2.90	0.004
Central	chitinase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.03	0.11	0.28	0.779	0.04	0.13	0.28	0.779
Central	chitinase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.24	0.09	-2.71	0.007	-0.36	0.12	-2.88	0.004
Central	chitinase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.03	0.11	0.27	0.784	0.01	0.14	0.10	0.920

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P*.std
Central	chitinase	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	chitinase	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	chitinase	pH	Chitinase	~	pH_historic	c	0.04	0.11	0.37	0.711	0.05	0.13	0.37	0.711
Central	chitinase	pH	Chitinase	~	pH_change	d	0.10	0.11	0.92	0.358	0.12	0.13	0.92	0.355
Central	chitinase	pH	Chitinase	~	LUI_historic	e	-0.22	0.09	-2.59	0.010	-0.34	0.12	-2.75	0.006
Central	chitinase	pH	Chitinase	~	LUI_change	f	0.04	0.11	0.33	0.742	0.04	0.13	0.33	0.742
Central	chitinase	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	chitinase	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	chitinase	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	chitinase	pH	Chitinase	~~	Chitinase		0.02	0.01	5.00	0.000	0.87	0.09	9.69	0.000
Central	chitinase	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	chitinase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.24	0.808	0.00	0.01	-0.24	0.808
Central	chitinase	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.02	-0.70	0.486	-0.02	0.03	-0.70	0.485
Central	chitinase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.23	0.09	-2.61	0.009	-0.34	0.12	-2.77	0.006
Central	chitinase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.02	0.11	0.19	0.847	0.03	0.13	0.19	0.847
Central	chitinase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.23	0.09	-2.61	0.009	-0.34	0.12	-2.76	0.006
Central	chitinase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.11	0.19	0.852	0.00	0.14	0.03	0.979
Central	urease	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.56	0.10	5.76	0.000	0.65	0.09	7.58	0.000
Central	urease	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.02	0.11	-0.14	0.888	-0.02	0.15	-0.14	0.888
Central	urease	CWM_leaf_P	Urease	~	CWM_leafP_historic	c	-0.50	0.18	-2.76	0.006	-0.47	0.16	-2.95	0.003
Central	urease	CWM_leaf_P	Urease	~	CWM_leafP_change	d	-0.29	0.20	-1.43	0.153	-0.18	0.13	-1.45	0.148
Central	urease	CWM_leaf_P	Urease	~	LUI_historic	e	-0.01	0.15	-0.09	0.929	-0.02	0.17	-0.09	0.929
Central	urease	CWM_leaf_P	Urease	~	LUI_change	f	-0.04	0.15	-0.25	0.802	-0.03	0.13	-0.25	0.802
Central	urease	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.30	0.768	0.04	0.15	0.30	0.767
Central	urease	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.74	0.000	0.58	0.11	5.15	0.000
Central	urease	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.01	4.74	0.000	1.00	0.01	159.30	0.000
Central	urease	CWM_leaf_P	Urease	~~	Urease		0.04	0.01	4.74	0.000	0.74	0.11	6.66	0.000
Central	urease	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	urease	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	urease	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.28	0.11	-2.49	0.013	-0.30	0.12	-2.65	0.008
Central	urease	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.03	0.14	0.888	0.00	0.03	0.14	0.888
Central	urease	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.29	0.13	-2.30	0.022	-0.32	0.13	-2.42	0.016
Central	urease	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.03	0.16	-0.22	0.829	-0.03	0.13	-0.22	0.829
Central	urease	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.29	0.13	-2.30	0.022	-0.32	0.13	-2.43	0.015
Central	urease	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.04	0.16	-0.22	0.825	-0.04	0.14	-0.30	0.761
Central	urease	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.13	0.13	-0.98	0.326	-0.15	0.15	-0.99	0.321
Central	urease	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.09	0.14	0.64	0.525	0.09	0.15	0.64	0.524
Central	urease	CWM_MycInt	Urease	~	CWM_MycInt_historic	c	-0.01	0.14	-0.03	0.974	-0.01	0.14	-0.03	0.974
Central	urease	CWM_MycInt	Urease	~	CWM_MycInt_change	d	0.16	0.18	0.88	0.377	0.12	0.14	0.89	0.374
Central	urease	CWM_MycInt	Urease	~	LUI_historic	e	-0.34	0.13	-2.67	0.008	-0.37	0.13	-2.87	0.004
Central	urease	CWM_MycInt	Urease	~	LUI_change	f	-0.08	0.17	-0.47	0.642	-0.06	0.14	-0.47	0.642
Central	urease	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.30	0.768	0.04	0.15	0.30	0.767
Central	urease	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.74	0.000	0.98	0.04	23.15	0.000
Central	urease	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.74	0.000	0.99	0.03	35.60	0.000
Central	urease	CWM_MycInt	Urease	~~	Urease		0.05	0.01	4.74	0.000	0.84	0.10	8.55	0.000
Central	urease	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	urease	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	urease	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.03	0.974	0.00	0.02	0.03	0.974
Central	urease	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.03	0.52	0.606	0.01	0.02	0.52	0.606
Central	urease	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.34	0.13	-2.70	0.007	-0.37	0.13	-2.90	0.004
Central	urease	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.06	0.17	-0.38	0.704	-0.05	0.14	-0.38	0.704
Central	urease	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.34	0.13	-2.70	0.007	-0.37	0.13	-2.92	0.004
Central	urease	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.06	0.17	-0.39	0.700	-0.07	0.15	-0.46	0.643
Central	urease	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.22	0.826	0.03	0.15	0.22	0.826
Central	urease	Plant_biomass	Plant_biomass	~	LUI_change	b	0.03	0.16	0.19	0.853	0.03	0.15	0.19	0.853
Central	urease	Plant_biomass	Urease	~	Plant_biomass	c	0.03	0.16	0.18	0.860	0.03	0.14	0.18	0.860
Central	urease	Plant_biomass	Urease	~	LUI_historic	e	-0.29	0.13	-2.28	0.023	-0.32	0.13	-2.40	0.016
Central	urease	Plant_biomass	Urease	~	LUI_change	f	-0.07	0.17	-0.41	0.684	-0.06	0.14	-0.41	0.683
Central	urease	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.30	0.768	0.04	0.15	0.30	0.767
Central	urease	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	4.74	0.000	1.00	0.01	76.48	0.000
Central	urease	Plant_biomass	Urease	~~	Urease		0.05	0.01	4.74	0.000	0.89	0.09	10.21	0.000
Central	urease	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	urease	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	urease	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.14	0.891	0.00	0.01	0.14	0.891
Central	urease	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.13	0.898	0.00	0.01	0.13	0.898
Central	urease	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.29	0.13	-2.27	0.023	-0.32	0.13	-2.40	0.017
Central	urease	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.07	0.17	-0.40	0.687	-0.06	0.14	-0.40	0.687
Central	urease	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.29	0.13	-2.27	0.023	-0.32	0.13	-2.42	0.016
Central	urease	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.07	0.17	-0.41	0.684	-0.07	0.15	-0.48	0.633

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
Central	urease	Lignin_content	Lignin_content	~	LUI_historic	a	0.11	0.13	0.84	0.401	0.12	0.15	0.85	0.397
Central	urease	Lignin_content	Lignin_content	~	LUI_change	b	0.05	0.17	0.29	0.775	0.04	0.15	0.29	0.774
Central	urease	Lignin_content	Urease	~	Lignin_content	c	0.40	0.14	2.91	0.004	0.38	0.12	3.09	0.002
Central	urease	Lignin_content	Urease	~	LUI_historic	e	-0.33	0.12	-2.82	0.005	-0.37	0.12	-2.98	0.003
Central	urease	Lignin_content	Urease	~	LUI_change	f	-0.09	0.15	-0.56	0.574	-0.07	0.13	-0.56	0.573
Central	urease	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.30	0.768	0.04	0.15	0.30	0.767
Central	urease	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.74	0.000	0.98	0.04	25.21	0.000
Central	urease	Lignin_content	Urease	~~	Urease		0.04	0.01	4.74	0.000	0.75	0.11	6.73	0.000
Central	urease	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	urease	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	urease	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.04	0.05	0.81	0.419	0.05	0.06	0.80	0.424
Central	urease	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.07	0.29	0.776	0.02	0.06	0.29	0.776
Central	urease	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.29	0.13	-2.27	0.023	-0.32	0.13	-2.40	0.017
Central	urease	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.07	0.17	-0.40	0.687	-0.06	0.14	-0.40	0.687
Central	urease	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.29	0.13	-2.27	0.023	-0.32	0.13	-2.42	0.016
Central	urease	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.07	0.17	-0.41	0.684	-0.07	0.15	-0.48	0.633
Central	urease	pH	pH_historic	~	LUI_historic	a	-0.06	0.12	-0.51	0.612	-0.08	0.15	-0.51	0.611
Central	urease	pH	pH_change	~	LUI_change	b	-0.13	0.15	-0.91	0.365	-0.13	0.15	-0.91	0.361
Central	urease	pH	Urease	~	pH_historic	c	0.10	0.15	0.66	0.510	0.09	0.14	0.66	0.508
Central	urease	pH	Urease	~	pH_change	d	0.11	0.17	0.66	0.507	0.09	0.14	0.67	0.505
Central	urease	pH	Urease	~	LUI_historic	e	-0.28	0.13	-2.18	0.030	-0.31	0.13	-2.28	0.022
Central	urease	pH	Urease	~	LUI_change	f	-0.07	0.17	-0.45	0.657	-0.06	0.14	-0.45	0.656
Central	urease	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.30	0.768	0.04	0.15	0.30	0.767
Central	urease	pH	pH_historic	~~	pH_historic		0.05	0.01	4.74	0.000	0.99	0.02	44.47	0.000
Central	urease	pH	pH_change	~~	pH_change		0.04	0.01	4.74	0.000	0.98	0.04	25.07	0.000
Central	urease	pH	Urease	~~	Urease		0.05	0.01	4.74	0.000	0.88	0.09	9.63	0.000
Central	urease	pH	LUI_historic	~~	LUI_historic		0.07	0.02	4.74	0.000	1.00	0.00	NA	NA
Central	urease	pH	LUI_change	~~	LUI_change		0.04	0.01	4.74	0.000	1.00	0.00	NA	NA
Central	urease	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.02	-0.40	0.688	-0.01	0.02	-0.40	0.687
Central	urease	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.03	-0.54	0.592	-0.01	0.02	-0.54	0.591
Central	urease	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.28	0.13	-2.22	0.026	-0.31	0.13	-2.34	0.019
Central	urease	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.09	0.17	-0.54	0.592	-0.08	0.14	-0.54	0.591
Central	urease	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.28	0.13	-2.22	0.026	-0.32	0.13	-2.36	0.018
Central	urease	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.17	-0.54	0.589	-0.09	0.15	-0.60	0.546
Central	DEA	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	DEA	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	DEA	CWM_leaf_P	DEA	~	CWM_leafP_historic	c	0.14	0.13	1.13	0.257	0.20	0.17	1.15	0.252
Central	DEA	CWM_leaf_P	DEA	~	CWM_leafP_change	d	0.03	0.14	0.25	0.807	0.03	0.13	0.25	0.807
Central	DEA	CWM_leaf_P	DEA	~	LUI_historic	e	-0.21	0.11	-1.98	0.047	-0.35	0.17	-2.05	0.040
Central	DEA	CWM_leaf_P	DEA	~	LUI_change	f	0.15	0.11	1.39	0.163	0.19	0.13	1.42	0.156
Central	DEA	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	DEA	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	DEA	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	DEA	CWM_leaf_P	DEA	~~	DEA		0.02	0.00	5.00	0.000	0.90	0.08	11.14	0.000
Central	DEA	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.08	0.07	1.11	0.266	0.13	0.11	1.12	0.262
Central	DEA	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.22	0.829	0.00	0.01	-0.22	0.829
Central	DEA	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.08	-1.61	0.106	-0.22	0.13	-1.65	0.098
Central	DEA	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.15	0.11	1.38	0.167	0.19	0.13	1.40	0.161
Central	DEA	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.13	0.08	-1.61	0.108	-0.21	0.14	-1.54	0.125
Central	DEA	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.15	0.11	1.38	0.169	0.17	0.14	1.26	0.206
Central	DEA	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	DEA	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	DEA	CWM_MycInt	DEA	~	CWM_MycInt_historic	c	-0.02	0.09	-0.26	0.798	-0.04	0.14	-0.26	0.798
Central	DEA	CWM_MycInt	DEA	~	CWM_MycInt_change	d	-0.01	0.12	-0.12	0.901	-0.02	0.14	-0.12	0.901
Central	DEA	CWM_MycInt	DEA	~	LUI_historic	e	-0.13	0.08	-1.60	0.111	-0.22	0.13	-1.63	0.102
Central	DEA	CWM_MycInt	DEA	~	LUI_change	f	0.15	0.11	1.43	0.152	0.20	0.13	1.46	0.145
Central	DEA	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	DEA	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	DEA	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	DEA	CWM_MycInt	DEA	~~	DEA		0.02	0.00	5.00	0.000	0.92	0.07	12.52	0.000
Central	DEA	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.25	0.806	0.00	0.02	0.25	0.806
Central	DEA	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.11	0.909	0.00	0.01	-0.11	0.909
Central	DEA	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.08	-1.58	0.115	-0.21	0.13	-1.61	0.107
Central	DEA	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.15	0.11	1.43	0.153	0.19	0.13	1.45	0.146
Central	DEA	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.13	0.08	-1.57	0.116	-0.20	0.14	-1.49	0.137
Central	DEA	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.15	0.11	1.42	0.155	0.18	0.14	1.32	0.187

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
Central	DEA	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	DEA	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	DEA	Plant_biomass	DEA	~	Plant_biomass	c	0.34	0.09	3.88	0.000	0.47	0.11	4.32	0.000
Central	DEA	Plant_biomass	DEA	~	LUI_historic	e	-0.14	0.07	-1.98	0.048	-0.24	0.12	-2.01	0.044
Central	DEA	Plant_biomass	DEA	~	LUI_change	f	0.11	0.09	1.12	0.262	0.14	0.12	1.13	0.259
Central	DEA	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	DEA	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	DEA	Plant_biomass	DEA	~~	DEA		0.02	0.00	5.00	0.000	0.71	0.11	6.53	0.000
Central	DEA	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.04	0.23	0.821	0.02	0.07	0.23	0.821
Central	DEA	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.04	0.05	0.85	0.397	0.06	0.07	0.86	0.390
Central	DEA	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.08	-1.62	0.104	-0.22	0.13	-1.66	0.096
Central	DEA	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.15	0.11	1.41	0.159	0.19	0.13	1.44	0.151
Central	DEA	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.13	0.08	-1.62	0.106	-0.21	0.14	-1.54	0.123
Central	DEA	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.15	0.11	1.41	0.160	0.18	0.14	1.30	0.195
Central	DEA	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	DEA	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	DEA	Lignin_content	DEA	~	Lignin_content	c	0.05	0.09	0.55	0.581	0.08	0.14	0.55	0.580
Central	DEA	Lignin_content	DEA	~	LUI_historic	e	-0.14	0.08	-1.67	0.095	-0.23	0.13	-1.71	0.087
Central	DEA	Lignin_content	DEA	~	LUI_change	f	0.15	0.11	1.38	0.169	0.19	0.13	1.40	0.162
Central	DEA	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	DEA	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	DEA	Lignin_content	DEA	~~	DEA		0.02	0.00	5.00	0.000	0.91	0.08	12.09	0.000
Central	DEA	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.41	0.685	0.01	0.02	0.41	0.684
Central	DEA	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.36	0.722	0.01	0.01	0.36	0.722
Central	DEA	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.08	-1.62	0.104	-0.22	0.13	-1.66	0.096
Central	DEA	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.15	0.11	1.41	0.159	0.19	0.13	1.44	0.151
Central	DEA	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.13	0.08	-1.62	0.106	-0.21	0.14	-1.54	0.123
Central	DEA	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.15	0.11	1.41	0.160	0.18	0.14	1.30	0.195
Central	DEA	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	DEA	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	DEA	pH	DEA	~	pH_historic	c	-0.06	0.10	-0.60	0.548	-0.08	0.13	-0.60	0.547
Central	DEA	pH	DEA	~	pH_change	d	-0.04	0.10	-0.37	0.712	-0.05	0.14	-0.37	0.712
Central	DEA	pH	DEA	~	LUI_historic	e	-0.14	0.08	-1.71	0.088	-0.23	0.13	-1.75	0.080
Central	DEA	pH	DEA	~	LUI_change	f	0.16	0.11	1.47	0.140	0.20	0.13	1.50	0.133
Central	DEA	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	DEA	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	DEA	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	DEA	pH	DEA	~~	DEA		0.02	0.00	5.00	0.000	0.90	0.08	11.35	0.000
Central	DEA	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	DEA	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.28	0.776	0.00	0.01	0.28	0.776
Central	DEA	pH	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.02	0.35	0.727	0.01	0.02	0.35	0.727
Central	DEA	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.14	0.08	-1.67	0.094	-0.23	0.13	-1.72	0.086
Central	DEA	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.16	0.11	1.54	0.123	0.21	0.13	1.58	0.115
Central	DEA	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.14	0.08	-1.67	0.095	-0.21	0.14	-1.58	0.114
Central	DEA	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.16	0.11	1.54	0.123	0.19	0.14	1.43	0.153
Central	phosphatase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	phosphatase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	phosphatase	CWM_leaf_P	Phosphatase	~	CWM_leafP_historic	c	-0.08	0.13	-0.58	0.563	-0.10	0.17	-0.58	0.562
Central	phosphatase	CWM_leaf_P	Phosphatase	~	CWM_leafP_change	d	-0.25	0.15	-1.73	0.084	-0.23	0.13	-1.77	0.077
Central	phosphatase	CWM_leaf_P	Phosphatase	~	LUI_historic	e	-0.17	0.11	-1.50	0.133	-0.25	0.17	-1.53	0.126
Central	phosphatase	CWM_leaf_P	Phosphatase	~	LUI_change	f	0.07	0.11	0.60	0.548	0.08	0.13	0.60	0.547
Central	phosphatase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	phosphatase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	phosphatase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	phosphatase	CWM_leaf_P	Phosphatase	~~	Phosphatase		0.02	0.01	5.00	0.000	0.84	0.09	8.99	0.000
Central	phosphatase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.04	0.07	-0.58	0.565	-0.06	0.11	-0.58	0.564
Central	phosphatase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.03	0.44	0.658	0.02	0.03	0.44	0.657
Central	phosphatase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.21	0.09	-2.42	0.016	-0.32	0.12	-2.54	0.011
Central	phosphatase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.08	0.11	0.69	0.488	0.09	0.13	0.70	0.487
Central	phosphatase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.21	0.09	-2.41	0.016	-0.31	0.13	-2.48	0.013
Central	phosphatase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.08	0.11	0.69	0.492	0.07	0.14	0.52	0.605

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
Central	phosphatase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	phosphatase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	phosphatase	CWM_MycInt	Phosphatase	~	CWM_MycInt_historic	c	-0.06	0.10	-0.57	0.570	-0.08	0.13	-0.57	0.569
Central	phosphatase	CWM_MycInt	Phosphatase	~	CWM_MycInt_change	d	-0.01	0.12	-0.07	0.945	-0.01	0.13	-0.07	0.945
Central	phosphatase	CWM_MycInt	Phosphatase	~	LUI_historic	e	-0.21	0.09	-2.36	0.018	-0.32	0.13	-2.48	0.013
Central	phosphatase	CWM_MycInt	Phosphatase	~	LUI_change	f	0.08	0.11	0.72	0.473	0.10	0.13	0.72	0.472
Central	phosphatase	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	phosphatase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	phosphatase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	phosphatase	CWM_MycInt	Phosphatase	~~	Phosphatase		0.03	0.01	5.00	0.000	0.89	0.08	10.84	0.000
Central	phosphatase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.01	0.48	0.633	0.01	0.02	0.48	0.633
Central	phosphatase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.07	0.946	0.00	0.01	-0.07	0.946
Central	phosphatase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.09	-2.30	0.022	-0.31	0.13	-2.41	0.016
Central	phosphatase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.08	0.11	0.72	0.475	0.10	0.13	0.72	0.473
Central	phosphatase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.20	0.09	-2.29	0.022	-0.30	0.13	-2.36	0.019
Central	phosphatase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.08	0.11	0.71	0.478	0.08	0.14	0.54	0.588
Central	phosphatase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	phosphatase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	phosphatase	Plant_biomass	Phosphatase	~	Plant_biomass	c	0.18	0.10	1.71	0.087	0.23	0.13	1.75	0.080
Central	phosphatase	Plant_biomass	Phosphatase	~	LUI_historic	e	-0.21	0.09	-2.44	0.015	-0.32	0.12	-2.57	0.010
Central	phosphatase	Plant_biomass	Phosphatase	~	LUI_change	f	0.05	0.11	0.48	0.635	0.06	0.13	0.48	0.634
Central	phosphatase	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	phosphatase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	phosphatase	Plant_biomass	Phosphatase	~~	Phosphatase		0.02	0.01	5.00	0.000	0.85	0.09	9.08	0.000
Central	phosphatase	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.23	0.822	0.01	0.03	0.22	0.822
Central	phosphatase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.03	0.78	0.439	0.03	0.04	0.78	0.436
Central	phosphatase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.09	-2.32	0.020	-0.31	0.13	-2.44	0.015
Central	phosphatase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.08	0.11	0.67	0.503	0.09	0.13	0.67	0.502
Central	phosphatase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.20	0.09	-2.32	0.020	-0.31	0.13	-2.39	0.017
Central	phosphatase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.08	0.11	0.66	0.507	0.07	0.14	0.50	0.619
Central	phosphatase	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	phosphatase	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	phosphatase	Lignin_content	Phosphatase	~	Lignin_content	c	0.12	0.10	1.21	0.225	0.16	0.13	1.23	0.220
Central	phosphatase	Lignin_content	Phosphatase	~	LUI_historic	e	-0.21	0.09	-2.45	0.014	-0.33	0.13	-2.58	0.010
Central	phosphatase	Lignin_content	Phosphatase	~	LUI_change	f	0.07	0.11	0.60	0.550	0.08	0.13	0.60	0.549
Central	phosphatase	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	phosphatase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	phosphatase	Lignin_content	Phosphatase	~~	Phosphatase		0.02	0.01	5.00	0.000	0.87	0.09	9.91	0.000
Central	phosphatase	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.54	0.591	0.01	0.03	0.54	0.591
Central	phosphatase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.43	0.664	0.01	0.02	0.44	0.664
Central	phosphatase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.09	-2.32	0.020	-0.31	0.13	-2.44	0.015
Central	phosphatase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.08	0.11	0.67	0.503	0.09	0.13	0.67	0.502
Central	phosphatase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.20	0.09	-2.32	0.020	-0.31	0.13	-2.39	0.017
Central	phosphatase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.08	0.11	0.66	0.507	0.07	0.14	0.50	0.619
Central	phosphatase	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	phosphatase	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	phosphatase	pH	Phosphatase	~	pH_historic	c	0.16	0.10	1.52	0.130	0.20	0.13	1.54	0.123
Central	phosphatase	pH	Phosphatase	~	pH_change	d	-0.07	0.10	-0.68	0.497	-0.09	0.13	-0.68	0.496
Central	phosphatase	pH	Phosphatase	~	LUI_historic	e	-0.20	0.08	-2.40	0.017	-0.31	0.13	-2.51	0.012
Central	phosphatase	pH	Phosphatase	~	LUI_change	f	0.03	0.11	0.26	0.792	0.04	0.13	0.26	0.792
Central	phosphatase	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	phosphatase	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	phosphatase	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	phosphatase	pH	Phosphatase	~~	Phosphatase		0.02	0.01	5.00	0.000	0.85	0.09	9.14	0.000
Central	phosphatase	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	phosphatase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.02	-0.32	0.753	-0.01	0.03	-0.32	0.752
Central	phosphatase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.02	0.57	0.567	0.01	0.02	0.57	0.566
Central	phosphatase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.21	0.09	-2.41	0.016	-0.32	0.13	-2.55	0.011
Central	phosphatase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.04	0.11	0.37	0.713	0.05	0.13	0.37	0.713
Central	phosphatase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.21	0.09	-2.41	0.016	-0.32	0.13	-2.52	0.012
Central	phosphatase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.04	0.11	0.36	0.718	0.03	0.14	0.20	0.842

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
Central	bacteria	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	bacteria	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	bacteria	CWM_leaf_P	bactotal	~	CWM_leafP_historic	c	0.05	0.18	0.30	0.764	0.05	0.18	0.30	0.764
Central	bacteria	CWM_leaf_P	bactotal	~	CWM_leafP_change	d	0.04	0.20	0.23	0.819	0.03	0.14	0.23	0.819
Central	bacteria	CWM_leaf_P	bactotal	~	LUI_historic	e	-0.05	0.15	-0.36	0.717	-0.07	0.18	-0.36	0.716
Central	bacteria	CWM_leaf_P	bactotal	~	LUI_change	f	0.22	0.15	1.51	0.131	0.21	0.14	1.54	0.123
Central	bacteria	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	bacteria	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	bacteria	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	bacteria	CWM_leaf_P	bactotal	~~	bactotal		0.04	0.01	5.00	0.000	0.95	0.06	16.53	0.000
Central	bacteria	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.09	0.30	0.765	0.03	0.11	0.30	0.764
Central	bacteria	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.20	0.838	0.00	0.01	-0.20	0.838
Central	bacteria	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.03	0.11	-0.22	0.824	-0.03	0.14	-0.22	0.824
Central	bacteria	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.22	0.15	1.50	0.135	0.21	0.14	1.53	0.126
Central	bacteria	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.02	0.11	-0.22	0.829	-0.02	0.14	-0.13	0.901
Central	bacteria	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.22	0.15	1.50	0.135	0.21	0.14	1.52	0.129
Central	bacteria	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	bacteria	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	bacteria	CWM_MycInt	bactotal	~	CWM_MycInt_historic	c	-0.26	0.12	-2.20	0.028	-0.27	0.12	-2.26	0.024
Central	bacteria	CWM_MycInt	bactotal	~	CWM_MycInt_change	d	0.35	0.15	2.37	0.018	0.29	0.12	2.46	0.014
Central	bacteria	CWM_MycInt	bactotal	~	LUI_historic	e	-0.15	0.10	-1.47	0.142	-0.18	0.12	-1.49	0.137
Central	bacteria	CWM_MycInt	bactotal	~	LUI_change	f	0.24	0.13	1.79	0.074	0.22	0.12	1.82	0.068
Central	bacteria	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	bacteria	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	bacteria	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	bacteria	CWM_MycInt	bactotal	~~	bactotal		0.04	0.01	5.00	0.000	0.77	0.10	7.52	0.000
Central	bacteria	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.03	0.82	0.415	0.03	0.04	0.82	0.415
Central	bacteria	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.05	0.29	0.770	0.01	0.04	0.29	0.769
Central	bacteria	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.12	0.11	-1.16	0.248	-0.15	0.13	-1.17	0.244
Central	bacteria	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.25	0.14	1.79	0.073	0.23	0.13	1.84	0.066
Central	bacteria	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.12	0.11	-1.15	0.251	-0.14	0.13	-1.02	0.309
Central	bacteria	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.25	0.14	1.79	0.074	0.23	0.13	1.74	0.082
Central	bacteria	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	bacteria	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	bacteria	Plant_biomass	bactotal	~	Plant_biomass	c	0.40	0.12	3.26	0.001	0.41	0.12	3.56	0.000
Central	bacteria	Plant_biomass	bactotal	~	LUI_historic	e	-0.04	0.10	-0.36	0.722	-0.05	0.13	-0.36	0.722
Central	bacteria	Plant_biomass	bactotal	~	LUI_change	f	0.17	0.13	1.25	0.211	0.16	0.13	1.26	0.207
Central	bacteria	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	bacteria	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	bacteria	Plant_biomass	bactotal	~~	bactotal		0.04	0.01	5.00	0.000	0.79	0.10	7.69	0.000
Central	bacteria	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.05	0.23	0.821	0.01	0.06	0.23	0.821
Central	bacteria	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.05	0.06	0.84	0.401	0.05	0.06	0.85	0.395
Central	bacteria	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.03	0.11	-0.23	0.819	-0.03	0.14	-0.23	0.819
Central	bacteria	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.22	0.15	1.51	0.132	0.21	0.14	1.54	0.123
Central	bacteria	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.03	0.11	-0.22	0.824	-0.02	0.14	-0.13	0.897
Central	bacteria	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.22	0.15	1.51	0.132	0.21	0.14	1.53	0.126
Central	bacteria	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	bacteria	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	bacteria	Lignin_content	bactotal	~	Lignin_content	c	0.12	0.13	0.94	0.349	0.13	0.14	0.95	0.345
Central	bacteria	Lignin_content	bactotal	~	LUI_historic	e	-0.04	0.11	-0.31	0.757	-0.04	0.14	-0.31	0.757
Central	bacteria	Lignin_content	bactotal	~	LUI_change	f	0.21	0.15	1.46	0.145	0.20	0.14	1.49	0.137
Central	bacteria	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	bacteria	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	bacteria	Lignin_content	bactotal	~~	bactotal		0.04	0.01	5.00	0.000	0.94	0.07	14.40	0.000
Central	bacteria	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.51	0.613	0.01	0.02	0.51	0.612
Central	bacteria	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.42	0.677	0.01	0.02	0.42	0.676
Central	bacteria	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.03	0.11	-0.23	0.819	-0.03	0.14	-0.23	0.819
Central	bacteria	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.22	0.15	1.51	0.132	0.21	0.14	1.54	0.123
Central	bacteria	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.03	0.11	-0.22	0.824	-0.02	0.14	-0.13	0.897
Central	bacteria	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.22	0.15	1.51	0.132	0.21	0.14	1.53	0.126

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
Central	bacteria	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	bacteria	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	bacteria	pH	bactotal	~	pH_historic	c	0.27	0.14	1.97	0.049	0.26	0.13	2.03	0.042
Central	bacteria	pH	bactotal	~	pH_change	d	0.12	0.14	0.89	0.376	0.12	0.13	0.89	0.373
Central	bacteria	pH	bactotal	~	LUI_historic	e	0.00	0.11	-0.01	0.991	0.00	0.13	-0.01	0.991
Central	bacteria	pH	bactotal	~	LUI_change	f	0.18	0.14	1.23	0.218	0.17	0.13	1.25	0.213
Central	bacteria	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	bacteria	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	bacteria	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	bacteria	pH	bactotal	~~	bactotal		0.04	0.01	5.00	0.000	0.90	0.08	11.03	0.000
Central	bacteria	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	bacteria	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.32	0.750	-0.01	0.04	-0.32	0.750
Central	bacteria	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.03	-0.68	0.495	-0.02	0.03	-0.68	0.494
Central	bacteria	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.01	0.11	-0.10	0.922	-0.01	0.14	-0.10	0.922
Central	bacteria	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.16	0.14	1.10	0.270	0.15	0.13	1.11	0.265
Central	bacteria	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.01	0.11	-0.09	0.926	0.00	0.14	-0.03	0.977
Central	bacteria	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.16	0.14	1.10	0.270	0.15	0.13	1.11	0.267
Central	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	CWM_leafP_historic	c	-0.11	0.16	-0.69	0.491	-0.11	0.15	-0.69	0.490
Central	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	CWM_leafP_change	d	-0.09	0.18	-0.50	0.616	-0.06	0.12	-0.50	0.615
Central	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	LUI_historic	e	-0.14	0.14	-1.02	0.310	-0.16	0.15	-1.02	0.308
Central	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	LUI_change	f	-0.55	0.14	-3.97	0.000	-0.47	0.11	-4.45	0.000
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~~	fungi_bac		0.04	0.01	5.00	0.000	0.71	0.11	6.54	0.000
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.06	0.09	-0.68	0.494	-0.07	0.10	-0.69	0.493
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.34	0.735	0.00	0.01	0.34	0.735
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.11	-1.87	0.061	-0.22	0.12	-1.91	0.056
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.54	0.14	-3.93	0.000	-0.47	0.11	-4.40	0.000
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.20	0.11	-1.89	0.059	-0.25	0.13	-1.93	0.054
Central	fungi:bacteria ratio	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.54	0.14	-3.94	0.000	-0.48	0.11	-4.48	0.000
Central	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	CWM_MycInt_historic	c	0.14	0.12	1.23	0.221	0.15	0.12	1.23	0.218
Central	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	CWM_MycInt_change	d	-0.09	0.15	-0.63	0.529	-0.07	0.12	-0.63	0.528
Central	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	LUI_historic	e	-0.16	0.11	-1.48	0.140	-0.18	0.12	-1.49	0.137
Central	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	LUI_change	f	-0.56	0.14	-4.11	0.000	-0.48	0.10	-4.63	0.000
Central	fungi:bacteria ratio	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~~	fungi_bac		0.04	0.01	5.00	0.000	0.69	0.11	6.39	0.000
Central	fungi:bacteria ratio	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.02	-0.71	0.476	-0.02	0.03	-0.72	0.473
Central	fungi:bacteria ratio	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.27	0.789	0.00	0.01	-0.27	0.789
Central	fungi:bacteria ratio	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.17	0.11	-1.61	0.107	-0.19	0.12	-1.63	0.102
Central	fungi:bacteria ratio	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.56	0.14	-4.12	0.000	-0.49	0.10	-4.66	0.000
Central	fungi:bacteria ratio	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.17	0.11	-1.63	0.103	-0.22	0.13	-1.67	0.095
Central	fungi:bacteria ratio	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.56	0.14	-4.13	0.000	-0.50	0.11	-4.74	0.000
Central	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	Plant_biomass	c	-0.17	0.13	-1.34	0.180	-0.16	0.12	-1.35	0.177
Central	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	LUI_historic	e	-0.19	0.11	-1.85	0.064	-0.22	0.12	-1.88	0.060
Central	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	LUI_change	f	-0.52	0.14	-3.83	0.000	-0.45	0.11	-4.23	0.000
Central	fungi:bacteria ratio	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	fungi:bacteria ratio	Plant_biomass	fungi_bac	~~	fungi_bac		0.04	0.01	5.00	0.000	0.69	0.11	6.34	0.000
Central	fungi:bacteria ratio	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.02	-0.22	0.823	-0.01	0.02	-0.22	0.823
Central	fungi:bacteria ratio	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.02	0.03	-0.73	0.466	-0.02	0.03	-0.74	0.462
Central	fungi:bacteria ratio	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.11	-1.86	0.063	-0.22	0.12	-1.89	0.058
Central	fungi:bacteria ratio	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.55	0.14	-3.95	0.000	-0.47	0.11	-4.44	0.000
Central	fungi:bacteria ratio	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.20	0.11	-1.88	0.061	-0.25	0.13	-1.91	0.056
Central	fungi:bacteria ratio	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.55	0.14	-3.95	0.000	-0.49	0.11	-4.51	0.000

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
Central	fungi:bacteria ratio	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	fungi:bacteria ratio	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	fungi:bacteria ratio	Lignin_content	fungi_bac	~	Lignin_content	c	0.15	0.12	1.23	0.220	0.15	0.12	1.23	0.217
Central	fungi:bacteria ratio	Lignin_content	fungi_bac	~	LUI_historic	e	-0.21	0.11	-1.99	0.047	-0.24	0.12	-2.02	0.043
Central	fungi:bacteria ratio	Lignin_content	fungi_bac	~	LUI_change	f	-0.56	0.14	-4.08	0.000	-0.48	0.11	-4.58	0.000
Central	fungi:bacteria ratio	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi:bacteria ratio	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	fungi:bacteria ratio	Lignin_content	fungi_bac	~~	fungi_bac		0.04	0.01	5.00	0.000	0.69	0.11	6.38	0.000
Central	fungi:bacteria ratio	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.54	0.590	0.01	0.02	0.54	0.590
Central	fungi:bacteria ratio	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.03	0.44	0.664	0.01	0.02	0.43	0.665
Central	fungi:bacteria ratio	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.11	-1.86	0.063	-0.22	0.12	-1.89	0.058
Central	fungi:bacteria ratio	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.55	0.14	-3.95	0.000	-0.47	0.11	-4.44	0.000
Central	fungi:bacteria ratio	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.20	0.11	-1.88	0.061	-0.25	0.13	-1.91	0.056
Central	fungi:bacteria ratio	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.55	0.14	-3.95	0.000	-0.49	0.11	-4.51	0.000
Central	fungi:bacteria ratio	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	fungi:bacteria ratio	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	fungi:bacteria ratio	pH	fungi_bac	~	pH_historic	c	0.10	0.13	0.78	0.434	0.09	0.12	0.79	0.433
Central	fungi:bacteria ratio	pH	fungi_bac	~	pH_change	d	-0.02	0.13	-0.12	0.908	-0.01	0.12	-0.12	0.908
Central	fungi:bacteria ratio	pH	fungi_bac	~	LUI_historic	e	-0.20	0.11	-1.84	0.066	-0.22	0.12	-1.87	0.062
Central	fungi:bacteria ratio	pH	fungi_bac	~	LUI_change	f	-0.57	0.14	-4.12	0.000	-0.49	0.11	-4.65	0.000
Central	fungi:bacteria ratio	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi:bacteria ratio	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	fungi:bacteria ratio	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	fungi:bacteria ratio	pH	fungi_bac	~~	fungi_bac		0.04	0.01	5.00	0.000	0.69	0.11	6.38	0.000
Central	fungi:bacteria ratio	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi:bacteria ratio	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.30	0.766	0.00	0.01	-0.30	0.765
Central	fungi:bacteria ratio	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.02	0.12	0.909	0.00	0.02	0.12	0.909
Central	fungi:bacteria ratio	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.20	0.11	-1.87	0.062	-0.22	0.12	-1.90	0.058
Central	fungi:bacteria ratio	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.57	0.14	-4.15	0.000	-0.49	0.10	-4.69	0.000
Central	fungi:bacteria ratio	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.20	0.11	-1.88	0.060	-0.25	0.13	-1.90	0.057
Central	fungi:bacteria ratio	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.57	0.14	-4.15	0.000	-0.50	0.11	-4.77	0.000
Central	fungi	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.53	0.09	5.84	0.000	0.64	0.08	7.58	0.000
Central	fungi	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.46	0.647	-0.07	0.14	-0.46	0.646
Central	fungi	CWM_leaf_P	fungi	~	CWM_leafP_historic	c	-0.03	0.17	-0.16	0.876	-0.03	0.17	-0.16	0.876
Central	fungi	CWM_leaf_P	fungi	~	CWM_leafP_change	d	0.03	0.19	0.18	0.855	0.02	0.13	0.18	0.855
Central	fungi	CWM_leaf_P	fungi	~	LUI_historic	e	-0.18	0.14	-1.25	0.212	-0.21	0.17	-1.26	0.207
Central	fungi	CWM_leaf_P	fungi	~	LUI_change	f	-0.29	0.14	-2.10	0.036	-0.28	0.13	-2.17	0.030
Central	fungi	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	5.00	0.000	0.59	0.11	5.55	0.000
Central	fungi	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.00	5.00	0.000	1.00	0.02	54.73	0.000
Central	fungi	CWM_leaf_P	fungi	~~	fungi		0.04	0.01	5.00	0.000	0.86	0.09	9.49	0.000
Central	fungi	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.09	-0.16	0.876	-0.02	0.11	-0.16	0.876
Central	fungi	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.17	0.866	0.00	0.01	-0.17	0.866
Central	fungi	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.19	0.11	-1.75	0.081	-0.23	0.13	-1.79	0.074
Central	fungi	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.30	0.14	-2.11	0.035	-0.28	0.13	-2.19	0.028
Central	fungi	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.19	0.11	-1.75	0.079	-0.25	0.13	-1.86	0.063
Central	fungi	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.30	0.14	-2.12	0.034	-0.29	0.13	-2.26	0.024
Central	fungi	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.11	0.13	-0.88	0.380	-0.12	0.14	-0.88	0.377
Central	fungi	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.13	0.30	0.768	0.04	0.14	0.30	0.768
Central	fungi	CWM_MycInt	fungi	~	CWM_MycInt_historic	c	-0.16	0.12	-1.35	0.176	-0.17	0.12	-1.37	0.172
Central	fungi	CWM_MycInt	fungi	~	CWM_MycInt_change	d	0.21	0.15	1.39	0.165	0.17	0.12	1.41	0.160
Central	fungi	CWM_MycInt	fungi	~	LUI_historic	e	-0.27	0.11	-2.52	0.012	-0.32	0.12	-2.63	0.008
Central	fungi	CWM_MycInt	fungi	~	LUI_change	f	-0.28	0.14	-2.11	0.035	-0.26	0.12	-2.17	0.030
Central	fungi	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	5.00	0.000	0.99	0.03	28.71	0.000
Central	fungi	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	1.00	0.01	84.79	0.000
Central	fungi	CWM_MycInt	fungi	~~	fungi		0.04	0.01	5.00	0.000	0.78	0.10	7.60	0.000
Central	fungi	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.02	0.74	0.462	0.02	0.03	0.74	0.462
Central	fungi	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.03	0.29	0.773	0.01	0.03	0.29	0.773
Central	fungi	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.25	0.11	-2.33	0.020	-0.30	0.12	-2.43	0.015
Central	fungi	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.28	0.14	-2.01	0.044	-0.26	0.12	-2.07	0.038
Central	fungi	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.25	0.11	-2.34	0.019	-0.31	0.13	-2.49	0.013
Central	fungi	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.28	0.14	-2.02	0.044	-0.28	0.13	-2.14	0.033

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
Central	fungi	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.03	0.12	0.23	0.821	0.03	0.14	0.23	0.821
Central	fungi	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.385	0.12	0.14	0.88	0.382
Central	fungi	Plant_biomass	fungi	~	Plant_biomass	c	0.23	0.13	1.82	0.069	0.23	0.13	1.86	0.063
Central	fungi	Plant_biomass	fungi	~	LUI_historic	e	-0.20	0.11	-1.86	0.063	-0.24	0.12	-1.91	0.057
Central	fungi	Plant_biomass	fungi	~	LUI_change	f	-0.33	0.14	-2.39	0.017	-0.31	0.12	-2.49	0.013
Central	fungi	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	5.00	0.000	0.98	0.04	27.60	0.000
Central	fungi	Plant_biomass	fungi	~~	fungi		0.04	0.01	5.00	0.000	0.81	0.10	8.07	0.000
Central	fungi	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.03	0.23	0.822	0.01	0.03	0.23	0.822
Central	fungi	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.03	0.04	0.78	0.433	0.03	0.04	0.78	0.434
Central	fungi	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.19	0.11	-1.75	0.081	-0.23	0.13	-1.79	0.073
Central	fungi	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.30	0.14	-2.12	0.034	-0.28	0.13	-2.20	0.028
Central	fungi	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.19	0.11	-1.76	0.079	-0.25	0.13	-1.87	0.062
Central	fungi	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.30	0.14	-2.12	0.034	-0.29	0.13	-2.27	0.023
Central	fungi	Lignin_content	Lignin_content	~	LUI_historic	a	0.07	0.12	0.60	0.548	0.09	0.14	0.60	0.547
Central	fungi	Lignin_content	Lignin_content	~	LUI_change	b	0.07	0.16	0.47	0.642	0.07	0.14	0.47	0.641
Central	fungi	Lignin_content	fungi	~	Lignin_content	c	0.09	0.12	0.74	0.458	0.10	0.13	0.75	0.456
Central	fungi	Lignin_content	fungi	~	LUI_historic	e	-0.20	0.11	-1.81	0.070	-0.24	0.13	-1.86	0.063
Central	fungi	Lignin_content	fungi	~	LUI_change	f	-0.30	0.14	-2.17	0.030	-0.29	0.13	-2.26	0.024
Central	fungi	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	5.00	0.000	0.99	0.03	32.09	0.000
Central	fungi	Lignin_content	fungi	~~	fungi		0.04	0.01	5.00	0.000	0.85	0.09	9.19	0.000
Central	fungi	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.47	0.641	0.01	0.02	0.47	0.640
Central	fungi	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.02	0.39	0.694	0.01	0.02	0.39	0.694
Central	fungi	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.19	0.11	-1.75	0.081	-0.23	0.13	-1.79	0.073
Central	fungi	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.30	0.14	-2.12	0.034	-0.28	0.13	-2.20	0.028
Central	fungi	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.19	0.11	-1.76	0.079	-0.25	0.13	-1.87	0.062
Central	fungi	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.30	0.14	-2.12	0.034	-0.29	0.13	-2.27	0.023
Central	fungi	pH	pH_historic	~	LUI_historic	a	-0.04	0.11	-0.32	0.747	-0.05	0.14	-0.32	0.747
Central	fungi	pH	pH_change	~	LUI_change	b	-0.16	0.15	-1.07	0.286	-0.15	0.14	-1.08	0.280
Central	fungi	pH	fungi	~	pH_historic	c	0.25	0.13	1.89	0.059	0.24	0.12	1.93	0.054
Central	fungi	pH	fungi	~	pH_change	d	0.06	0.13	0.43	0.670	0.05	0.13	0.43	0.670
Central	fungi	pH	fungi	~	LUI_historic	e	-0.17	0.11	-1.63	0.103	-0.20	0.12	-1.66	0.098
Central	fungi	pH	fungi	~	LUI_change	f	-0.34	0.14	-2.49	0.013	-0.32	0.12	-2.61	0.009
Central	fungi	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.45	0.652	0.06	0.14	0.45	0.650
Central	fungi	pH	pH_historic	~~	pH_historic		0.04	0.01	5.00	0.000	1.00	0.01	77.64	0.000
Central	fungi	pH	pH_change	~~	pH_change		0.04	0.01	5.00	0.000	0.98	0.04	23.68	0.000
Central	fungi	pH	fungi	~~	fungi		0.04	0.01	5.00	0.000	0.78	0.10	7.67	0.000
Central	fungi	pH	LUI_historic	~~	LUI_historic		0.07	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	pH	LUI_change	~~	LUI_change		0.04	0.01	5.00	0.000	1.00	0.00	NA	NA
Central	fungi	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.32	0.751	-0.01	0.03	-0.32	0.750
Central	fungi	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.02	-0.40	0.692	-0.01	0.02	-0.40	0.692
Central	fungi	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.18	0.11	-1.66	0.097	-0.22	0.13	-1.69	0.090
Central	fungi	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.35	0.14	-2.58	0.010	-0.32	0.12	-2.71	0.007
Central	fungi	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.18	0.11	-1.67	0.095	-0.24	0.13	-1.77	0.077
Central	fungi	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.35	0.14	-2.59	0.010	-0.34	0.12	-2.78	0.006
Central	ergosterol	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.54	0.10	5.66	0.000	0.64	0.09	7.34	0.000
Central	ergosterol	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.05	0.11	-0.48	0.633	-0.07	0.15	-0.48	0.632
Central	ergosterol	CWM_leaf_P	Ergosterol	~	CWM_leafP_historic	c	-0.21	0.18	-1.14	0.255	-0.21	0.18	-1.15	0.249
Central	ergosterol	CWM_leaf_P	Ergosterol	~	CWM_leafP_change	d	-0.08	0.20	-0.39	0.700	-0.05	0.14	-0.39	0.700
Central	ergosterol	CWM_leaf_P	Ergosterol	~	LUI_historic	e	-0.07	0.15	-0.45	0.651	-0.08	0.18	-0.45	0.651
Central	ergosterol	CWM_leaf_P	Ergosterol	~	LUI_change	f	0.08	0.16	0.49	0.628	0.07	0.14	0.49	0.627
Central	ergosterol	CWM_leaf_P	LUI_historic	~~	LUI_change	g	0.00	0.01	0.56	0.576	0.08	0.15	0.57	0.572
Central	ergosterol	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.03	0.01	4.85	0.000	0.60	0.11	5.39	0.000
Central	ergosterol	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.02	0.01	4.85	0.000	1.00	0.02	49.28	0.000
Central	ergosterol	CWM_leaf_P	Ergosterol	~~	Ergosterol		0.05	0.01	4.85	0.000	0.92	0.08	12.39	0.000
Central	ergosterol	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.07	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	CWM_leaf_P	LUI_change	~~	LUI_change		0.04	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.11	0.10	-1.12	0.264	-0.13	0.12	-1.13	0.258
Central	ergosterol	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.30	0.764	0.00	0.01	0.30	0.764
Central	ergosterol	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.18	0.12	-1.50	0.133	-0.21	0.14	-1.54	0.124
Central	ergosterol	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.08	0.15	0.51	0.608	0.07	0.14	0.51	0.608
Central	ergosterol	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.18	0.12	-1.50	0.134	-0.21	0.14	-1.49	0.135
Central	ergosterol	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.08	0.15	0.51	0.612	0.06	0.14	0.38	0.704

Table S6.2 continued

Region	**MO variable**	**mediator**	**lhs**	**op**	**rhs**	**label**	**est**	**se**	**z**	***P***	**est.std**	**se.std**	**z.std**	***P*.std**
Central	ergosterol	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	-0.13	0.13	-1.01	0.311	-0.15	0.14	-1.02	0.306
Central	ergosterol	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	0.04	0.14	0.27	0.790	0.04	0.15	0.27	0.790
Central	ergosterol	CWM_MycInt	Ergosterol	~	CWM_MycInt_historic	c	0.00	0.13	-0.03	0.977	0.00	0.14	-0.03	0.977
Central	ergosterol	CWM_MycInt	Ergosterol	~	CWM_MycInt_change	d	0.30	0.16	1.80	0.071	0.24	0.13	1.85	0.064
Central	ergosterol	CWM_MycInt	Ergosterol	~	LUI_historic	e	-0.27	0.12	-2.28	0.023	-0.31	0.13	-2.39	0.017
Central	ergosterol	CWM_MycInt	Ergosterol	~	LUI_change	f	0.07	0.15	0.47	0.640	0.06	0.13	0.47	0.640
Central	ergosterol	CWM_MycInt	LUI_historic	~~	LUI_change	g	0.00	0.01	0.56	0.576	0.08	0.15	0.57	0.572
Central	ergosterol	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.05	0.01	4.85	0.000	0.98	0.04	23.44	0.000
Central	ergosterol	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.04	0.01	4.85	0.000	1.00	0.01	88.40	0.000
Central	ergosterol	CWM_MycInt	Ergosterol	~~	Ergosterol		0.04	0.01	4.85	0.000	0.84	0.10	8.84	0.000
Central	ergosterol	CWM_MycInt	LUI_historic	~~	LUI_historic		0.07	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	CWM_MycInt	LUI_change	~~	LUI_change		0.04	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.03	0.977	0.00	0.02	0.03	0.977
Central	ergosterol	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.04	0.26	0.792	0.01	0.04	0.26	0.792
Central	ergosterol	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.27	0.12	-2.30	0.021	-0.31	0.13	-2.41	0.016
Central	ergosterol	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.08	0.16	0.52	0.603	0.07	0.14	0.52	0.602
Central	ergosterol	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.27	0.12	-2.30	0.021	-0.30	0.13	-2.36	0.018
Central	ergosterol	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.08	0.16	0.51	0.608	0.05	0.15	0.32	0.747
Central	ergosterol	Plant_biomass	Plant_biomass	~	LUI_historic	a	-0.01	0.12	-0.07	0.944	-0.01	0.15	-0.07	0.944
Central	ergosterol	Plant_biomass	Plant_biomass	~	LUI_change	b	0.13	0.15	0.87	0.383	0.13	0.14	0.88	0.379
Central	ergosterol	Plant_biomass	Ergosterol	~	Plant_biomass	c	0.14	0.15	0.95	0.344	0.14	0.14	0.96	0.340
Central	ergosterol	Plant_biomass	Ergosterol	~	LUI_historic	e	-0.18	0.12	-1.50	0.132	-0.21	0.14	-1.54	0.124
Central	ergosterol	Plant_biomass	Ergosterol	~	LUI_change	f	0.05	0.16	0.34	0.734	0.05	0.14	0.34	0.733
Central	ergosterol	Plant_biomass	LUI_historic	~~	LUI_change	g	0.00	0.01	0.56	0.576	0.08	0.15	0.57	0.572
Central	ergosterol	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.04	0.01	4.85	0.000	0.98	0.04	27.15	0.000
Central	ergosterol	Plant_biomass	Ergosterol	~~	Ergosterol		0.05	0.01	4.85	0.000	0.93	0.07	13.37	0.000
Central	ergosterol	Plant_biomass	LUI_historic	~~	LUI_historic		0.07	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	Plant_biomass	LUI_change	~~	LUI_change		0.04	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.07	0.944	0.00	0.02	-0.07	0.944
Central	ergosterol	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.03	0.64	0.521	0.02	0.03	0.64	0.519
Central	ergosterol	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.18	0.12	-1.50	0.134	-0.21	0.14	-1.54	0.125
Central	ergosterol	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.07	0.16	0.46	0.646	0.07	0.14	0.46	0.646
Central	ergosterol	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.18	0.12	-1.50	0.134	-0.21	0.14	-1.50	0.134
Central	ergosterol	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.07	0.16	0.45	0.650	0.05	0.15	0.33	0.741
Central	ergosterol	Lignin_content	Lignin_content	~	LUI_historic	a	0.06	0.13	0.49	0.622	0.07	0.15	0.49	0.622
Central	ergosterol	Lignin_content	Lignin_content	~	LUI_change	b	0.11	0.17	0.65	0.515	0.09	0.15	0.65	0.514
Central	ergosterol	Lignin_content	Ergosterol	~	Lignin_content	c	0.30	0.13	2.27	0.023	0.31	0.13	2.37	0.018
Central	ergosterol	Lignin_content	Ergosterol	~	LUI_historic	e	-0.20	0.11	-1.74	0.082	-0.24	0.13	-1.78	0.075
Central	ergosterol	Lignin_content	Ergosterol	~	LUI_change	f	0.04	0.15	0.27	0.789	0.04	0.14	0.27	0.789
Central	ergosterol	Lignin_content	LUI_historic	~~	LUI_change	g	0.00	0.01	0.56	0.576	0.08	0.15	0.57	0.572
Central	ergosterol	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.85	0.000	0.99	0.04	27.85	0.000
Central	ergosterol	Lignin_content	Ergosterol	~~	Ergosterol		0.04	0.01	4.85	0.000	0.86	0.09	9.11	0.000
Central	ergosterol	Lignin_content	LUI_historic	~~	LUI_historic		0.07	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	Lignin_content	LUI_change	~~	LUI_change		0.04	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.04	0.48	0.630	0.02	0.05	0.48	0.631
Central	ergosterol	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.03	0.05	0.63	0.532	0.03	0.05	0.63	0.530
Central	ergosterol	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.18	0.12	-1.50	0.134	-0.21	0.14	-1.54	0.125
Central	ergosterol	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.07	0.16	0.46	0.646	0.07	0.14	0.46	0.646
Central	ergosterol	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.18	0.12	-1.50	0.134	-0.21	0.14	-1.50	0.134
Central	ergosterol	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.07	0.16	0.45	0.650	0.05	0.15	0.33	0.741
Central	ergosterol	pH	pH_historic	~	LUI_historic	a	-0.02	0.12	-0.15	0.883	-0.02	0.15	-0.15	0.883
Central	ergosterol	pH	pH_change	~	LUI_change	b	-0.20	0.15	-1.35	0.178	-0.19	0.14	-1.37	0.170
Central	ergosterol	pH	Ergosterol	~	pH_historic	c	0.29	0.15	1.97	0.048	0.27	0.13	2.04	0.041
Central	ergosterol	pH	Ergosterol	~	pH_change	d	0.15	0.15	1.02	0.307	0.14	0.14	1.03	0.303
Central	ergosterol	pH	Ergosterol	~	LUI_historic	e	-0.16	0.12	-1.36	0.174	-0.19	0.14	-1.38	0.167
Central	ergosterol	pH	Ergosterol	~	LUI_change	f	0.05	0.16	0.32	0.751	0.04	0.14	0.32	0.751
Central	ergosterol	pH	LUI_historic	~~	LUI_change	g	0.00	0.01	0.56	0.576	0.08	0.15	0.57	0.572
Central	ergosterol	pH	pH_historic	~~	pH_historic		0.04	0.01	4.85	0.000	1.00	0.01	159.91	0.000
Central	ergosterol	pH	pH_change	~~	pH_change		0.04	0.01	4.85	0.000	0.96	0.05	17.77	0.000
Central	ergosterol	pH	Ergosterol	~~	Ergosterol		0.04	0.01	4.85	0.000	0.87	0.09	9.66	0.000
Central	ergosterol	pH	LUI_historic	~~	LUI_historic		0.07	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	pH	LUI_change	~~	LUI_change		0.04	0.01	4.85	0.000	1.00	0.00	NA	NA
Central	ergosterol	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.15	0.883	-0.01	0.04	-0.15	0.883
Central	ergosterol	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.03	0.04	-0.81	0.416	-0.03	0.03	-0.82	0.413
Central	ergosterol	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.16	0.12	-1.35	0.177	-0.19	0.14	-1.37	0.170
Central	ergosterol	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.02	0.15	0.12	0.903	0.02	0.14	0.12	0.903
Central	ergosterol	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.16	0.12	-1.35	0.177	-0.19	0.14	-1.37	0.171
Central	ergosterol	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.02	0.15	0.12	0.907	0.00	0.14	0.01	0.994

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
North-East	Cmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	Cmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	Cmic	CWM_leaf_P	Cmic	~	CWM_leafP_historic	c	-0.09	0.13	-0.64	0.520	-0.09	0.14	-0.65	0.518
North-East	Cmic	CWM_leaf_P	Cmic	~	CWM_leafP_change	d	0.05	0.14	0.35	0.726	0.05	0.15	0.35	0.726
North-East	Cmic	CWM_leaf_P	Cmic	~	LUI_historic	e	0.03	0.11	0.31	0.754	0.05	0.16	0.31	0.753
North-East	Cmic	CWM_leaf_P	Cmic	~	LUI_change	f	0.02	0.19	0.11	0.915	0.02	0.16	0.11	0.915
North-East	Cmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Cmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	Cmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	Cmic	CWM_leaf_P	Cmic	~~	Cmic		0.04	0.01	5.00	0.000	0.99	0.03	31.73	0.000
North-East	Cmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.29	0.773	0.00	0.01	-0.29	0.773
North-East	Cmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.04	-0.34	0.731	-0.01	0.04	-0.34	0.731
North-East	Cmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.03	0.11	0.29	0.774	0.05	0.16	0.29	0.774
North-East	Cmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.01	0.18	0.03	0.976	0.01	0.16	0.03	0.976
North-East	Cmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.03	0.11	0.29	0.772	0.04	0.14	0.30	0.762
North-East	Cmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.01	0.18	0.03	0.978	-0.02	0.14	-0.10	0.918
North-East	Cmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	Cmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	Cmic	CWM_MycInt	Cmic	~	CWM_MycInt_historic	c	0.37	0.14	2.56	0.010	0.33	0.12	2.68	0.007
North-East	Cmic	CWM_MycInt	Cmic	~	CWM_MycInt_change	d	0.39	0.15	2.64	0.008	0.33	0.12	2.77	0.006
North-East	Cmic	CWM_MycInt	Cmic	~	LUI_historic	e	0.01	0.11	0.12	0.908	0.02	0.14	0.12	0.908
North-East	Cmic	CWM_MycInt	Cmic	~	LUI_change	f	-0.03	0.18	-0.19	0.852	-0.03	0.14	-0.19	0.852
North-East	Cmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Cmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	Cmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	Cmic	CWM_MycInt	Cmic	~~	Cmic		0.04	0.01	5.00	0.000	0.77	0.10	7.60	0.000
North-East	Cmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.06	0.04	1.43	0.154	0.08	0.05	1.45	0.146
North-East	Cmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.06	0.06	-0.95	0.344	-0.05	0.05	-0.96	0.340
North-East	Cmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.11	0.65	0.519	0.09	0.14	0.65	0.517
North-East	Cmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.09	0.19	-0.50	0.617	-0.07	0.15	-0.50	0.616
North-East	Cmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.07	0.11	0.67	0.501	0.13	0.13	0.94	0.348
North-East	Cmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.09	0.18	-0.51	0.609	-0.11	0.13	-0.85	0.398
North-East	Cmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	Cmic	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	Cmic	Plant_biomass	Cmic	~	Plant_biomass	c	0.40	0.12	3.37	0.001	0.45	0.12	3.73	0.000
North-East	Cmic	Plant_biomass	Cmic	~	LUI_historic	e	-0.05	0.10	-0.52	0.601	-0.08	0.15	-0.52	0.600
North-East	Cmic	Plant_biomass	Cmic	~	LUI_change	f	-0.04	0.17	-0.23	0.820	-0.03	0.14	-0.23	0.820
North-East	Cmic	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	Cmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	Cmic	Plant_biomass	Cmic	~~	Cmic		0.03	0.01	4.95	0.000	0.81	0.10	8.04	0.000
North-East	Cmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.08	0.05	1.45	0.147	0.11	0.08	1.47	0.141
North-East	Cmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.08	0.19	0.851	0.01	0.07	0.19	0.851
North-East	Cmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.02	0.11	0.21	0.833	0.03	0.16	0.21	0.833
North-East	Cmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.02	0.19	-0.12	0.902	-0.02	0.16	-0.12	0.902
North-East	Cmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.02	0.11	0.22	0.827	0.04	0.14	0.29	0.769
North-East	Cmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.02	0.19	-0.13	0.899	-0.03	0.14	-0.24	0.812
North-East	Cmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	Cmic	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	Cmic	Lignin_content	Cmic	~	Lignin_content	c	-0.10	0.13	-0.72	0.472	-0.11	0.15	-0.72	0.470
North-East	Cmic	Lignin_content	Cmic	~	LUI_historic	e	0.04	0.11	0.39	0.696	0.06	0.16	0.39	0.696
North-East	Cmic	Lignin_content	Cmic	~	LUI_change	f	0.00	0.19	-0.01	0.992	0.00	0.16	-0.01	0.992
North-East	Cmic	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	Cmic	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	Cmic	Lignin_content	Cmic	~~	Cmic		0.04	0.01	4.95	0.000	0.99	0.03	31.36	0.000
North-East	Cmic	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.03	-0.67	0.503	-0.03	0.05	-0.67	0.501
North-East	Cmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.02	0.04	-0.60	0.546	-0.02	0.03	-0.61	0.544
North-East	Cmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.02	0.11	0.21	0.833	0.03	0.16	0.21	0.833
North-East	Cmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.02	0.19	-0.12	0.902	-0.02	0.16	-0.12	0.902
North-East	Cmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.02	0.11	0.22	0.827	0.04	0.14	0.29	0.769
North-East	Cmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.02	0.19	-0.13	0.899	-0.03	0.14	-0.24	0.812

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P*.std
North-East	Cmic	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	Cmic	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	Cmic	pH	Cmic	~	pH_historic	c	-0.13	0.09	-1.50	0.134	-0.21	0.13	-1.53	0.126
North-East	Cmic	pH	Cmic	~	pH_change	d	0.17	0.23	0.74	0.459	0.10	0.14	0.74	0.457
North-East	Cmic	pH	Cmic	~	LUI_historic	e	0.02	0.11	0.18	0.860	0.03	0.15	0.18	0.860
North-East	Cmic	pH	Cmic	~	LUI_change	f	-0.07	0.18	-0.36	0.717	-0.06	0.15	-0.36	0.717
North-East	Cmic	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Cmic	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	Cmic	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	Cmic	pH	Cmic	~~	Cmic		0.04	0.01	5.00	0.000	0.94	0.06	14.83	0.000
North-East	Cmic	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.13	0.897	0.00	0.03	0.13	0.897
North-East	Cmic	pH	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.02	0.35	0.723	0.01	0.02	0.36	0.723
North-East	Cmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.02	0.11	0.20	0.844	0.03	0.16	0.20	0.844
North-East	Cmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.06	0.18	-0.32	0.746	-0.05	0.15	-0.32	0.746
North-East	Cmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.02	0.11	0.21	0.833	0.05	0.14	0.37	0.712
North-East	Cmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.06	0.18	-0.33	0.743	-0.06	0.14	-0.45	0.651
North-East	Nmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	Nmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	Nmic	CWM_leaf_P	Nmic	~	CWM_leafP_historic	c	0.03	0.13	0.24	0.807	0.03	0.14	0.24	0.807
North-East	Nmic	CWM_leaf_P	Nmic	~	CWM_leafP_change	d	0.12	0.13	0.86	0.388	0.13	0.14	0.87	0.384
North-East	Nmic	CWM_leaf_P	Nmic	~	LUI_historic	e	0.04	0.11	0.36	0.718	0.06	0.16	0.36	0.718
North-East	Nmic	CWM_leaf_P	Nmic	~	LUI_change	f	0.03	0.18	0.16	0.876	0.03	0.16	0.16	0.876
North-East	Nmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Nmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	Nmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	Nmic	CWM_leaf_P	Nmic	~~	Nmic		0.04	0.01	5.00	0.000	0.98	0.04	25.41	0.000
North-East	Nmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Nmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Nmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.20	0.846	0.00	0.01	0.20	0.846
North-East	Nmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.04	0.05	-0.78	0.438	-0.03	0.04	-0.78	0.435
North-East	Nmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.04	0.11	0.37	0.711	0.06	0.16	0.37	0.710
North-East	Nmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.01	0.18	-0.04	0.972	-0.01	0.16	-0.04	0.972
North-East	Nmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.04	0.10	0.38	0.706	0.06	0.14	0.43	0.669
North-East	Nmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.01	0.18	-0.04	0.968	-0.03	0.14	-0.22	0.830
North-East	Nmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	Nmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	Nmic	CWM_MycInt	Nmic	~	CWM_MycInt_historic	c	0.15	0.15	1.03	0.303	0.15	0.14	1.04	0.298
North-East	Nmic	CWM_MycInt	Nmic	~	CWM_MycInt_change	d	0.09	0.15	0.58	0.559	0.08	0.14	0.59	0.558
North-East	Nmic	CWM_MycInt	Nmic	~	LUI_historic	e	0.02	0.11	0.17	0.864	0.03	0.16	0.17	0.864
North-East	Nmic	CWM_MycInt	Nmic	~	LUI_change	f	-0.03	0.18	-0.15	0.878	-0.02	0.16	-0.15	0.878
North-East	Nmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Nmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	Nmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	Nmic	CWM_MycInt	Nmic	~~	Nmic		0.04	0.01	5.00	0.000	0.97	0.05	19.21	0.000
North-East	Nmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Nmic	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Nmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.03	0.88	0.377	0.04	0.04	0.89	0.373
North-East	Nmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.03	-0.51	0.613	-0.01	0.02	-0.51	0.612
North-East	Nmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.04	0.11	0.40	0.691	0.06	0.16	0.40	0.690
North-East	Nmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.04	0.18	-0.23	0.819	-0.04	0.15	-0.23	0.819
North-East	Nmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.04	0.11	0.41	0.680	0.08	0.14	0.55	0.583
North-East	Nmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.04	0.18	-0.24	0.814	-0.06	0.14	-0.44	0.657
North-East	Nmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	Nmic	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	Nmic	Plant_biomass	Nmic	~	Plant_biomass	c	0.32	0.12	2.69	0.007	0.37	0.13	2.88	0.004
North-East	Nmic	Plant_biomass	Nmic	~	LUI_historic	e	-0.02	0.10	-0.23	0.817	-0.04	0.15	-0.23	0.817
North-East	Nmic	Plant_biomass	Nmic	~	LUI_change	f	-0.01	0.17	-0.08	0.939	-0.01	0.15	-0.08	0.939
North-East	Nmic	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	Nmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	Nmic	Plant_biomass	Nmic	~~	Nmic		0.03	0.01	4.95	0.000	0.87	0.09	9.66	0.000
North-East	Nmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	Nmic	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	Nmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.06	0.05	1.38	0.168	0.09	0.07	1.40	0.161
North-East	Nmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.07	0.19	0.851	0.01	0.06	0.19	0.851
North-East	Nmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.04	0.11	0.35	0.724	0.06	0.16	0.35	0.723
North-East	Nmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.00	0.18	0.00	0.997	0.00	0.16	0.00	0.997
North-East	Nmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.04	0.11	0.36	0.719	0.06	0.14	0.39	0.694
North-East	Nmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.00	0.18	-0.01	0.994	-0.03	0.14	-0.17	0.863

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
North-East	Nmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	Nmic	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	Nmic	Lignin_content	Nmic	~	Lignin_content	c	0.05	0.13	0.42	0.676	0.06	0.15	0.42	0.676
North-East	Nmic	Lignin_content	Nmic	~	LUI_historic	e	0.03	0.11	0.24	0.814	0.04	0.16	0.24	0.814
North-East	Nmic	Lignin_content	Nmic	~	LUI_change	f	-0.01	0.18	-0.07	0.945	-0.01	0.16	-0.07	0.945
North-East	Nmic	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	Nmic	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	Nmic	Lignin_content	Nmic	~~	Nmic		0.04	0.01	4.95	0.000	0.99	0.02	42.81	0.000
North-East	Nmic	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	Nmic	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	Nmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.03	0.41	0.684	0.02	0.04	0.41	0.683
North-East	Nmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.03	0.39	0.696	0.01	0.03	0.39	0.695
North-East	Nmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.04	0.11	0.35	0.724	0.06	0.16	0.35	0.723
North-East	Nmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.00	0.18	0.00	0.997	0.00	0.16	0.00	0.997
North-East	Nmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.04	0.11	0.36	0.719	0.06	0.14	0.39	0.694
North-East	Nmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.00	0.18	-0.01	0.994	-0.03	0.14	-0.17	0.863
North-East	Nmic	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	Nmic	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	Nmic	pH	Nmic	~	pH_historic	c	0.00	0.08	-0.05	0.962	-0.01	0.14	-0.05	0.962
North-East	Nmic	pH	Nmic	~	pH_change	d	0.45	0.22	2.01	0.044	0.27	0.13	2.09	0.037
North-East	Nmic	pH	Nmic	~	LUI_historic	e	0.06	0.10	0.60	0.549	0.09	0.15	0.60	0.548
North-East	Nmic	pH	Nmic	~	LUI_change	f	0.00	0.17	-0.01	0.990	0.00	0.15	-0.01	0.990
North-East	Nmic	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Nmic	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	Nmic	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	Nmic	pH	Nmic	~~	Nmic		0.04	0.01	5.00	0.000	0.92	0.07	12.41	0.000
North-East	Nmic	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Nmic	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Nmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	0.05	0.964	0.00	0.00	0.05	0.964
North-East	Nmic	pH	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.05	0.40	0.692	0.02	0.04	0.40	0.692
North-East	Nmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.10	0.60	0.548	0.09	0.15	0.60	0.547
North-East	Nmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.02	0.18	0.09	0.930	0.01	0.16	0.09	0.930
North-East	Nmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.06	0.10	0.61	0.545	0.08	0.14	0.62	0.536
North-East	Nmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.01	0.18	0.08	0.935	-0.03	0.14	-0.18	0.859
North-East	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	CWM_leafP_historic	c	-0.04	0.10	-0.41	0.681	-0.05	0.13	-0.41	0.681
North-East	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	CWM_leafP_change	d	-0.16	0.11	-1.53	0.126	-0.21	0.13	-1.56	0.119
North-East	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	LUI_historic	e	-0.11	0.09	-1.27	0.205	-0.19	0.14	-1.28	0.199
North-East	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~	LUI_change	f	-0.37	0.15	-2.50	0.012	-0.38	0.14	-2.64	0.008
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	Cmic:Nmic ratio	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	Cmic:Nmic ratio	CWM_leaf_P	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.02	0.01	5.00	0.000	0.87	0.09	9.80	0.000
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.25	0.800	0.00	0.01	-0.25	0.799
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.05	0.04	1.16	0.247	0.05	0.04	1.16	0.244
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.11	0.09	-1.28	0.199	-0.19	0.14	-1.30	0.194
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.32	0.15	-2.18	0.029	-0.32	0.14	-2.28	0.023
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.10	0.08	-1.22	0.221	-0.05	0.14	-0.35	0.729
North-East	Cmic:Nmic ratio	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.32	0.15	-2.18	0.030	-0.24	0.13	-1.83	0.067
North-East	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	CWM_MycInt_historic	c	0.06	0.12	0.50	0.617	0.07	0.14	0.50	0.616
North-East	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	CWM_MycInt_change	d	0.02	0.12	0.18	0.859	0.02	0.14	0.18	0.859
North-East	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	LUI_historic	e	-0.12	0.09	-1.33	0.182	-0.20	0.15	-1.35	0.176
North-East	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~	LUI_change	f	-0.34	0.15	-2.33	0.020	-0.35	0.14	-2.44	0.015
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	Cmic:Nmic ratio	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	Cmic:Nmic ratio	CWM_MycInt	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.03	0.01	5.00	0.000	0.89	0.08	10.86	0.000
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.48	0.631	0.02	0.03	0.48	0.631
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.02	-0.18	0.861	0.00	0.02	-0.18	0.861
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.11	0.09	-1.25	0.210	-0.19	0.15	-1.27	0.204
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.34	0.15	-2.37	0.018	-0.35	0.14	-2.49	0.013
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.10	0.09	-1.19	0.235	-0.04	0.14	-0.25	0.805
North-East	Cmic:Nmic ratio	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.34	0.15	-2.37	0.018	-0.27	0.13	-2.07	0.038

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
North-East	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	Plant_biomass	c	-0.18	0.10	-1.73	0.083	-0.24	0.13	-1.77	0.076
North-East	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	LUI_historic	e	-0.07	0.09	-0.85	0.396	-0.13	0.15	-0.85	0.394
North-East	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~	LUI_change	f	-0.32	0.14	-2.24	0.025	-0.33	0.14	-2.33	0.020
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	Cmic:Nmic ratio	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	Cmic:Nmic ratio	Plant_biomass	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.02	0.01	4.95	0.000	0.86	0.09	9.19	0.000
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.03	0.03	-1.18	0.239	-0.06	0.05	-1.20	0.232
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.04	-0.19	0.851	-0.01	0.04	-0.19	0.851
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.11	0.09	-1.23	0.219	-0.19	0.15	-1.25	0.213
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.33	0.15	-2.22	0.027	-0.33	0.14	-2.32	0.020
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.10	0.09	-1.17	0.243	-0.04	0.14	-0.29	0.770
North-East	Cmic:Nmic ratio	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.32	0.15	-2.21	0.027	-0.25	0.13	-1.90	0.057
North-East	Cmic:Nmic ratio	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	Cmic:Nmic ratio	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	Lignin_content	c	0.01	0.11	0.12	0.906	0.02	0.14	0.12	0.906
North-East	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	LUI_historic	e	-0.11	0.09	-1.22	0.223	-0.19	0.15	-1.24	0.217
North-East	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~	LUI_change	f	-0.33	0.15	-2.21	0.027	-0.34	0.15	-2.31	0.021
North-East	Cmic:Nmic ratio	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	Cmic:Nmic ratio	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	Cmic:Nmic ratio	Lignin_content	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.03	0.01	4.95	0.000	0.91	0.08	11.48	0.000
North-East	Cmic:Nmic ratio	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.12	0.906	0.01	0.04	0.12	0.906
North-East	Cmic:Nmic ratio	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.02	0.12	0.906	0.00	0.02	0.12	0.906
North-East	Cmic:Nmic ratio	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.11	0.09	-1.23	0.219	-0.19	0.15	-1.25	0.213
North-East	Cmic:Nmic ratio	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.33	0.15	-2.22	0.027	-0.33	0.14	-2.32	0.020
North-East	Cmic:Nmic ratio	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.10	0.09	-1.17	0.243	-0.04	0.14	-0.29	0.770
North-East	Cmic:Nmic ratio	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.32	0.15	-2.21	0.027	-0.25	0.13	-1.90	0.057
North-East	Cmic:Nmic ratio	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	Cmic:Nmic ratio	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	pH_historic	c	0.02	0.06	0.28	0.777	0.03	0.12	0.28	0.777
North-East	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	pH_change	d	-0.66	0.16	-4.13	0.000	-0.48	0.10	-4.60	0.000
North-East	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	LUI_historic	e	-0.14	0.07	-1.90	0.058	-0.24	0.13	-1.92	0.055
North-East	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~	LUI_change	f	-0.32	0.13	-2.55	0.011	-0.33	0.12	-2.62	0.009
North-East	Cmic:Nmic ratio	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	Cmic:Nmic ratio	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	Cmic:Nmic ratio	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	Cmic:Nmic ratio	pH	RatioCmic_Nmic	~~	RatioCmic_Nmic		0.02	0.00	5.00	0.000	0.66	0.11	6.20	0.000
North-East	Cmic:Nmic ratio	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	Cmic:Nmic ratio	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	-0.12	0.906	0.00	0.01	-0.12	0.906
North-East	Cmic:Nmic ratio	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.03	0.07	-0.40	0.688	-0.03	0.07	-0.41	0.686
North-East	Cmic:Nmic ratio	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.14	0.07	-1.90	0.057	-0.24	0.13	-1.93	0.054
North-East	Cmic:Nmic ratio	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.35	0.14	-2.45	0.014	-0.35	0.14	-2.56	0.010
North-East	Cmic:Nmic ratio	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.13	0.07	-1.83	0.068	-0.09	0.13	-0.71	0.476
North-East	Cmic:Nmic ratio	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.34	0.14	-2.44	0.015	-0.25	0.13	-1.87	0.061
North-East	Pmic	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	-0.01	0.11	-0.05	0.958	-0.01	0.15	-0.05	0.958
North-East	Pmic	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.36	0.18	-2.04	0.042	-0.29	0.14	-2.13	0.034
North-East	Pmic	CWM_leaf_P	Pmic	~	CWM_leafP_historic	c	0.13	0.14	0.90	0.366	0.12	0.14	0.91	0.363
North-East	Pmic	CWM_leaf_P	Pmic	~	CWM_leafP_change	d	-0.34	0.14	-2.35	0.019	-0.33	0.14	-2.47	0.013
North-East	Pmic	CWM_leaf_P	Pmic	~	LUI_historic	e	-0.01	0.11	-0.09	0.926	-0.01	0.15	-0.09	0.926
North-East	Pmic	CWM_leaf_P	Pmic	~	LUI_change	f	0.09	0.20	0.46	0.646	0.07	0.15	0.46	0.646
North-East	Pmic	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.55	0.011	-0.41	0.12	-3.30	0.001
North-East	Pmic	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	4.80	0.000	1.00	0.00	432.79	0.000
North-East	Pmic	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	4.80	0.000	0.92	0.08	11.80	0.000
North-East	Pmic	CWM_leaf_P	Pmic	~~	Pmic		0.04	0.01	4.80	0.000	0.85	0.10	8.90	0.000
North-East	Pmic	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	4.80	0.000	1.00	0.00	NA	NA
North-East	Pmic	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	4.80	0.000	1.00	0.00	NA	NA
North-East	Pmic	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.05	0.958	0.00	0.02	-0.05	0.958
North-East	Pmic	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.12	0.08	1.54	0.124	0.10	0.06	1.58	0.113
North-East	Pmic	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.01	0.11	-0.10	0.922	-0.02	0.15	-0.10	0.922
North-East	Pmic	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.21	0.20	1.07	0.286	0.17	0.15	1.08	0.280
North-East	Pmic	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.02	0.11	-0.14	0.891	-0.08	0.14	-0.59	0.556
North-East	Pmic	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.21	0.20	1.07	0.283	0.17	0.14	1.22	0.224

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
North-East	Pmic	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.20	0.09	2.20	0.028	0.31	0.13	2.31	0.021
North-East	Pmic	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.12	0.15	-0.80	0.421	-0.12	0.15	-0.81	0.418
North-East	Pmic	CWM_MycInt	Pmic	~	CWM_MycInt_historic	c	-0.19	0.16	-1.16	0.247	-0.15	0.13	-1.17	0.244
North-East	Pmic	CWM_MycInt	Pmic	~	CWM_MycInt_change	d	-0.64	0.17	-3.91	0.000	-0.48	0.11	-4.38	0.000
North-East	Pmic	CWM_MycInt	Pmic	~	LUI_historic	e	-0.11	0.12	-0.97	0.333	-0.13	0.14	-0.97	0.331
North-East	Pmic	CWM_MycInt	Pmic	~	LUI_change	f	0.13	0.19	0.71	0.477	0.10	0.13	0.71	0.476
North-East	Pmic	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.55	0.011	-0.41	0.12	-3.30	0.001
North-East	Pmic	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.03	0.01	4.80	0.000	0.91	0.08	11.00	0.000
North-East	Pmic	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	4.80	0.000	0.99	0.03	28.81	0.000
North-East	Pmic	CWM_MycInt	Pmic	~~	Pmic		0.04	0.01	4.80	0.000	0.68	0.11	6.08	0.000
North-East	Pmic	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	4.80	0.000	1.00	0.00	NA	NA
North-East	Pmic	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	4.80	0.000	1.00	0.00	NA	NA
North-East	Pmic	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.04	0.04	-1.03	0.305	-0.05	0.04	-1.03	0.302
North-East	Pmic	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.08	0.10	0.79	0.431	0.06	0.07	0.80	0.424
North-East	Pmic	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.15	0.11	-1.34	0.181	-0.18	0.13	-1.35	0.177
North-East	Pmic	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.21	0.21	1.01	0.314	0.15	0.15	1.02	0.308
North-East	Pmic	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.16	0.11	-1.39	0.164	-0.24	0.13	-1.93	0.053
North-East	Pmic	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.21	0.21	1.03	0.305	0.22	0.14	1.62	0.106
North-East	Pmic	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.17	0.12	1.40	0.161	0.22	0.16	1.43	0.152
North-East	Pmic	Plant_biomass	Plant_biomass	~	LUI_change	b	0.05	0.20	0.26	0.798	0.04	0.16	0.26	0.798
North-East	Pmic	Plant_biomass	Pmic	~	Plant_biomass	c	-0.14	0.14	-0.97	0.332	-0.14	0.15	-0.98	0.328
North-East	Pmic	Plant_biomass	Pmic	~	LUI_historic	e	0.03	0.12	0.22	0.829	0.04	0.16	0.22	0.829
North-East	Pmic	Plant_biomass	Pmic	~	LUI_change	f	0.28	0.20	1.41	0.159	0.22	0.16	1.44	0.151
North-East	Pmic	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.52	0.012	-0.41	0.13	-3.26	0.001
North-East	Pmic	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.74	0.000	0.96	0.06	15.95	0.000
North-East	Pmic	Plant_biomass	Pmic	~~	Pmic		0.04	0.01	4.74	0.000	0.93	0.07	13.07	0.000
North-East	Pmic	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.74	0.000	1.00	0.00	NA	NA
North-East	Pmic	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.74	0.000	1.00	0.00	NA	NA
North-East	Pmic	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.03	-0.80	0.425	-0.03	0.04	-0.80	0.422
North-East	Pmic	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.03	-0.25	0.805	-0.01	0.02	-0.25	0.805
North-East	Pmic	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.00	0.12	0.02	0.986	0.00	0.16	0.02	0.986
North-East	Pmic	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.27	0.20	1.36	0.174	0.22	0.16	1.39	0.166
North-East	Pmic	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.00	0.12	-0.03	0.977	-0.09	0.15	-0.57	0.566
North-East	Pmic	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.20	1.37	0.172	0.22	0.14	1.51	0.130
North-East	Pmic	Lignin_content	Lignin_content	~	LUI_historic	a	0.27	0.12	2.16	0.031	0.34	0.15	2.27	0.024
North-East	Pmic	Lignin_content	Lignin_content	~	LUI_change	b	0.20	0.21	0.99	0.322	0.15	0.15	1.00	0.318
North-East	Pmic	Lignin_content	Pmic	~	Lignin_content	c	0.25	0.14	1.79	0.074	0.26	0.14	1.85	0.065
North-East	Pmic	Lignin_content	Pmic	~	LUI_historic	e	-0.06	0.12	-0.53	0.596	-0.09	0.16	-0.53	0.595
North-East	Pmic	Lignin_content	Pmic	~	LUI_change	f	0.22	0.19	1.13	0.259	0.18	0.15	1.14	0.253
North-East	Pmic	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.52	0.012	-0.41	0.13	-3.26	0.001
North-East	Pmic	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.74	0.000	0.91	0.08	10.93	0.000
North-East	Pmic	Lignin_content	Pmic	~~	Pmic		0.04	0.01	4.74	0.000	0.89	0.09	10.13	0.000
North-East	Pmic	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.74	0.000	1.00	0.00	NA	NA
North-East	Pmic	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.74	0.000	1.00	0.00	NA	NA
North-East	Pmic	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.07	0.05	1.38	0.168	0.09	0.06	1.40	0.161
North-East	Pmic	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.05	0.06	0.87	0.386	0.04	0.05	0.88	0.380
North-East	Pmic	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.00	0.12	0.02	0.986	0.00	0.16	0.02	0.986
North-East	Pmic	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.27	0.20	1.36	0.174	0.22	0.16	1.39	0.166
North-East	Pmic	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.00	0.12	-0.03	0.977	-0.09	0.15	-0.57	0.566
North-East	Pmic	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.20	1.37	0.172	0.22	0.14	1.51	0.130
North-East	Pmic	pH	pH_historic	~	LUI_historic	a	-0.05	0.16	-0.28	0.782	-0.04	0.15	-0.28	0.782
North-East	Pmic	pH	pH_change	~	LUI_change	b	0.02	0.11	0.22	0.825	0.03	0.15	0.22	0.825
North-East	Pmic	pH	Pmic	~	pH_historic	c	0.21	0.10	2.19	0.029	0.29	0.13	2.28	0.023
North-East	Pmic	pH	Pmic	~	pH_change	d	0.35	0.25	1.39	0.166	0.19	0.13	1.41	0.160
North-East	Pmic	pH	Pmic	~	LUI_historic	e	0.04	0.12	0.36	0.718	0.05	0.15	0.36	0.717
North-East	Pmic	pH	Pmic	~	LUI_change	f	0.32	0.20	1.61	0.108	0.24	0.14	1.64	0.101
North-East	Pmic	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.55	0.011	-0.41	0.12	-3.30	0.001
North-East	Pmic	pH	pH_historic	~~	pH_historic		0.10	0.02	4.80	0.000	1.00	0.01	83.21	0.000
North-East	Pmic	pH	pH_change	~~	pH_change		0.02	0.00	4.80	0.000	1.00	0.01	104.10	0.000
North-East	Pmic	pH	Pmic	~~	Pmic		0.04	0.01	4.80	0.000	0.83	0.10	8.34	0.000
North-East	Pmic	pH	LUI_historic	~~	LUI_historic		0.08	0.02	4.80	0.000	1.00	0.00	NA	NA
North-East	Pmic	pH	LUI_change	~~	LUI_change		0.03	0.01	4.80	0.000	1.00	0.00	NA	NA
North-East	Pmic	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.04	-0.27	0.784	-0.01	0.04	-0.28	0.783
North-East	Pmic	pH	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.04	0.22	0.827	0.01	0.03	0.22	0.827
North-East	Pmic	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.03	0.12	0.27	0.788	0.04	0.15	0.27	0.788
North-East	Pmic	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.32	0.20	1.62	0.105	0.24	0.15	1.66	0.098
North-East	Pmic	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.03	0.12	0.22	0.827	-0.06	0.15	-0.39	0.694
North-East	Pmic	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.32	0.20	1.62	0.105	0.23	0.14	1.67	0.095

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
North-East	beta-glucosidase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	beta-glucosidase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	beta-glucosidase	CWM_leaf_P	Glucosidase	~	CWM_leafP_historic	c	0.03	0.14	0.25	0.804	0.03	0.14	0.25	0.804
North-East	beta-glucosidase	CWM_leaf_P	Glucosidase	~	CWM_leafP_change	d	0.05	0.14	0.37	0.708	0.05	0.14	0.38	0.708
North-East	beta-glucosidase	CWM_leaf_P	Glucosidase	~	LUI_historic	e	0.05	0.11	0.48	0.631	0.07	0.15	0.48	0.630
North-East	beta-glucosidase	CWM_leaf_P	Glucosidase	~	LUI_change	f	0.29	0.19	1.51	0.132	0.24	0.15	1.54	0.123
North-East	beta-glucosidase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	beta-glucosidase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	beta-glucosidase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	beta-glucosidase	CWM_leaf_P	Glucosidase	~~	Glucosidase		0.04	0.01	5.00	0.000	0.96	0.06	16.66	0.000
North-East	beta-glucosidase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.20	0.844	0.00	0.01	0.20	0.844
North-East	beta-glucosidase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.04	-0.37	0.714	-0.01	0.04	-0.37	0.714
North-East	beta-glucosidase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.11	0.49	0.623	0.08	0.15	0.49	0.622
North-East	beta-glucosidase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.28	0.19	1.46	0.144	0.22	0.15	1.49	0.136
North-East	beta-glucosidase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.11	0.45	0.656	-0.02	0.14	-0.15	0.881
North-East	beta-glucosidase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.19	1.46	0.144	0.19	0.14	1.41	0.160
North-East	beta-glucosidase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	beta-glucosidase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	beta-glucosidase	CWM_MycInt	Glucosidase	~	CWM_MycInt_historic	c	0.20	0.15	1.35	0.177	0.19	0.14	1.37	0.170
North-East	beta-glucosidase	CWM_MycInt	Glucosidase	~	CWM_MycInt_change	d	-0.15	0.16	-0.97	0.332	-0.13	0.14	-0.98	0.328
North-East	beta-glucosidase	CWM_MycInt	Glucosidase	~	LUI_historic	e	-0.03	0.11	-0.23	0.819	-0.04	0.15	-0.23	0.819
North-East	beta-glucosidase	CWM_MycInt	Glucosidase	~	LUI_change	f	0.17	0.18	0.91	0.364	0.14	0.15	0.92	0.360
North-East	beta-glucosidase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	beta-glucosidase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	beta-glucosidase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	beta-glucosidase	CWM_MycInt	Glucosidase	~~	Glucosidase		0.04	0.01	5.00	0.000	0.93	0.07	13.06	0.000
North-East	beta-glucosidase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.03	1.06	0.289	0.05	0.04	1.07	0.285
North-East	beta-glucosidase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.03	0.70	0.484	0.02	0.03	0.70	0.481
North-East	beta-glucosidase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.01	0.11	0.06	0.952	0.01	0.15	0.06	0.952
North-East	beta-glucosidase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.19	0.18	1.03	0.301	0.16	0.15	1.04	0.297
North-East	beta-glucosidase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.00	0.11	0.02	0.981	-0.06	0.14	-0.42	0.676
North-East	beta-glucosidase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.19	0.18	1.04	0.299	0.15	0.14	1.12	0.261
North-East	beta-glucosidase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	beta-glucosidase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	beta-glucosidase	Plant_biomass	Glucosidase	~	Plant_biomass	c	0.05	0.13	0.40	0.687	0.06	0.14	0.40	0.687
North-East	beta-glucosidase	Plant_biomass	Glucosidase	~	LUI_historic	e	0.05	0.12	0.40	0.692	0.06	0.16	0.40	0.692
North-East	beta-glucosidase	Plant_biomass	Glucosidase	~	LUI_change	f	0.29	0.19	1.50	0.134	0.23	0.15	1.53	0.126
North-East	beta-glucosidase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	beta-glucosidase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	beta-glucosidase	Plant_biomass	Glucosidase	~~	Glucosidase		0.04	0.01	4.95	0.000	0.95	0.06	15.98	0.000
North-East	beta-glucosidase	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.03	0.39	0.696	0.01	0.04	0.39	0.696
North-East	beta-glucosidase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.17	0.864	0.00	0.01	0.17	0.864
North-East	beta-glucosidase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.11	0.50	0.619	0.08	0.15	0.50	0.618
North-East	beta-glucosidase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.29	0.19	1.51	0.132	0.23	0.15	1.54	0.123
North-East	beta-glucosidase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.05	0.11	0.45	0.653	-0.02	0.14	-0.16	0.870
North-East	beta-glucosidase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.29	0.19	1.51	0.131	0.20	0.14	1.46	0.145
North-East	beta-glucosidase	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	beta-glucosidase	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	beta-glucosidase	Lignin_content	Glucosidase	~	Lignin_content	c	0.07	0.14	0.52	0.603	0.08	0.14	0.52	0.602
North-East	beta-glucosidase	Lignin_content	Glucosidase	~	LUI_historic	e	0.04	0.12	0.35	0.727	0.06	0.16	0.35	0.727
North-East	beta-glucosidase	Lignin_content	Glucosidase	~	LUI_change	f	0.27	0.19	1.41	0.158	0.22	0.15	1.44	0.150
North-East	beta-glucosidase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	beta-glucosidase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	beta-glucosidase	Lignin_content	Glucosidase	~~	Glucosidase		0.04	0.01	4.95	0.000	0.95	0.06	15.64	0.000
North-East	beta-glucosidase	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.03	0.50	0.617	0.02	0.04	0.50	0.616
North-East	beta-glucosidase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.02	0.03	0.47	0.638	0.01	0.03	0.47	0.637
North-East	beta-glucosidase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.11	0.50	0.619	0.08	0.15	0.50	0.618
North-East	beta-glucosidase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.29	0.19	1.51	0.132	0.23	0.15	1.54	0.123
North-East	beta-glucosidase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.05	0.11	0.45	0.653	-0.02	0.14	-0.16	0.870
North-East	beta-glucosidase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.29	0.19	1.51	0.131	0.20	0.14	1.46	0.145

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
North-East	beta-glucosidase	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	beta-glucosidase	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	beta-glucosidase	pH	Glucosidase	~	pH_historic	c	-0.09	0.08	-1.17	0.243	-0.14	0.12	-1.17	0.240
North-East	beta-glucosidase	pH	Glucosidase	~	pH_change	d	0.80	0.20	3.91	0.000	0.47	0.11	4.38	0.000
North-East	beta-glucosidase	pH	Glucosidase	~	LUI_historic	e	0.09	0.09	0.94	0.350	0.12	0.13	0.94	0.348
North-East	beta-glucosidase	pH	Glucosidase	~	LUI_change	f	0.25	0.16	1.57	0.116	0.21	0.13	1.59	0.112
North-East	beta-glucosidase	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	beta-glucosidase	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	beta-glucosidase	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	beta-glucosidase	pH	Glucosidase	~~	Glucosidase		0.03	0.01	5.00	0.000	0.72	0.11	6.73	0.000
North-East	beta-glucosidase	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-glucosidase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.13	0.898	0.00	0.02	0.13	0.898
North-East	beta-glucosidase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.03	0.08	0.40	0.688	0.03	0.07	0.40	0.686
North-East	beta-glucosidase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.09	0.10	0.94	0.345	0.13	0.13	0.95	0.343
North-East	beta-glucosidase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.28	0.18	1.59	0.112	0.24	0.15	1.62	0.105
North-East	beta-glucosidase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.08	0.09	0.89	0.371	0.03	0.13	0.20	0.845
North-East	beta-glucosidase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.28	0.18	1.59	0.113	0.18	0.14	1.33	0.183
North-East	beta-xylosidase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	beta-xylosidase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	beta-xylosidase	CWM_leaf_P	Xylosidase	~	CWM_leafP_historic	c	0.10	0.13	0.77	0.444	0.11	0.14	0.77	0.442
North-East	beta-xylosidase	CWM_leaf_P	Xylosidase	~	CWM_leafP_change	d	0.03	0.13	0.23	0.820	0.03	0.14	0.23	0.820
North-East	beta-xylosidase	CWM_leaf_P	Xylosidase	~	LUI_historic	e	0.03	0.10	0.26	0.795	0.04	0.15	0.26	0.795
North-East	beta-xylosidase	CWM_leaf_P	Xylosidase	~	LUI_change	f	0.28	0.18	1.59	0.111	0.25	0.15	1.63	0.102
North-East	beta-xylosidase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	beta-xylosidase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	beta-xylosidase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	beta-xylosidase	CWM_leaf_P	Xylosidase	~~	Xylosidase		0.04	0.01	5.00	0.000	0.94	0.07	14.21	0.000
North-East	beta-xylosidase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.30	0.766	0.01	0.02	0.30	0.766
North-East	beta-xylosidase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.04	-0.23	0.822	-0.01	0.04	-0.23	0.822
North-East	beta-xylosidase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.03	0.10	0.29	0.772	0.04	0.15	0.29	0.772
North-East	beta-xylosidase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.28	0.17	1.58	0.114	0.24	0.15	1.62	0.105
North-East	beta-xylosidase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.02	0.10	0.24	0.812	-0.06	0.14	-0.42	0.674
North-East	beta-xylosidase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.17	1.59	0.112	0.22	0.13	1.65	0.099
North-East	beta-xylosidase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	beta-xylosidase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	beta-xylosidase	CWM_MycInt	Xylosidase	~	CWM_MycInt_historic	c	0.00	0.14	-0.02	0.981	0.00	0.13	-0.02	0.981
North-East	beta-xylosidase	CWM_MycInt	Xylosidase	~	CWM_MycInt_change	d	-0.32	0.14	-2.27	0.023	-0.30	0.13	-2.37	0.018
North-East	beta-xylosidase	CWM_MycInt	Xylosidase	~	LUI_historic	e	-0.03	0.10	-0.29	0.773	-0.04	0.15	-0.29	0.773
North-East	beta-xylosidase	CWM_MycInt	Xylosidase	~	LUI_change	f	0.21	0.17	1.22	0.222	0.18	0.14	1.24	0.217
North-East	beta-xylosidase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	beta-xylosidase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	beta-xylosidase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.94	0.000
North-East	beta-xylosidase	CWM_MycInt	Xylosidase	~~	Xylosidase		0.03	0.01	5.00	0.000	0.85	0.09	9.24	0.000
North-East	beta-xylosidase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	-0.02	0.981	0.00	0.03	-0.02	0.981
North-East	beta-xylosidase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.05	0.05	0.93	0.355	0.04	0.05	0.94	0.348
North-East	beta-xylosidase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.03	0.10	-0.30	0.764	-0.04	0.15	-0.30	0.764
North-East	beta-xylosidase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.25	0.17	1.46	0.143	0.22	0.15	1.49	0.135
North-East	beta-xylosidase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.04	0.10	-0.36	0.719	-0.14	0.13	-1.04	0.300
North-East	beta-xylosidase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.26	0.17	1.47	0.140	0.24	0.13	1.80	0.073
North-East	beta-xylosidase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	beta-xylosidase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	beta-xylosidase	Plant_biomass	Xylosidase	~	Plant_biomass	c	-0.04	0.12	-0.31	0.755	-0.04	0.14	-0.31	0.755
North-East	beta-xylosidase	Plant_biomass	Xylosidase	~	LUI_historic	e	0.04	0.11	0.41	0.681	0.07	0.16	0.41	0.680
North-East	beta-xylosidase	Plant_biomass	Xylosidase	~	LUI_change	f	0.31	0.18	1.75	0.081	0.27	0.15	1.80	0.072
North-East	beta-xylosidase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	beta-xylosidase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	beta-xylosidase	Plant_biomass	Xylosidase	~~	Xylosidase		0.04	0.01	4.95	0.000	0.94	0.07	13.91	0.000
North-East	beta-xylosidase	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.02	-0.31	0.759	-0.01	0.04	-0.31	0.759
North-East	beta-xylosidase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	-0.16	0.872	0.00	0.01	-0.16	0.872
North-East	beta-xylosidase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.04	0.10	0.35	0.726	0.05	0.15	0.35	0.726
North-East	beta-xylosidase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.31	0.18	1.74	0.082	0.27	0.15	1.79	0.074
North-East	beta-xylosidase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.03	0.10	0.29	0.770	-0.06	0.14	-0.43	0.668
North-East	beta-xylosidase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.31	0.18	1.74	0.082	0.24	0.13	1.81	0.070

Table S6.2 continued

Region	**MO variable**	**mediator**	**lhs**	**op**	**rhs**	**label**	**est**	**se**	**z**	***P***	**est.std**	**se.std**	**z.std**	***P*.std**
North-East	beta-xylosidase	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	beta-xylosidase	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	beta-xylosidase	Lignin_content	Xylosidase	~	Lignin_content	c	0.04	0.13	0.29	0.771	0.04	0.14	0.29	0.771
North-East	beta-xylosidase	Lignin_content	Xylosidase	~	LUI_historic	e	0.03	0.11	0.26	0.792	0.04	0.16	0.26	0.792
North-East	beta-xylosidase	Lignin_content	Xylosidase	~	LUI_change	f	0.30	0.18	1.67	0.095	0.26	0.15	1.72	0.086
North-East	beta-xylosidase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	beta-xylosidase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	beta-xylosidase	Lignin_content	Xylosidase	~~	Xylosidase		0.04	0.01	4.95	0.000	0.94	0.07	13.93	0.000
North-East	beta-xylosidase	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.03	0.29	0.773	0.01	0.04	0.29	0.773
North-East	beta-xylosidase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.03	0.28	0.778	0.01	0.03	0.28	0.778
North-East	beta-xylosidase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.04	0.10	0.35	0.726	0.05	0.15	0.35	0.726
North-East	beta-xylosidase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.31	0.18	1.74	0.082	0.27	0.15	1.79	0.074
North-East	beta-xylosidase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.03	0.10	0.29	0.770	-0.06	0.14	-0.43	0.668
North-East	beta-xylosidase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.31	0.18	1.74	0.082	0.24	0.13	1.81	0.070
North-East	beta-xylosidase	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	beta-xylosidase	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	beta-xylosidase	pH	Xylosidase	~	pH_historic	c	0.05	0.08	0.59	0.557	0.07	0.13	0.59	0.556
North-East	beta-xylosidase	pH	Xylosidase	~	pH_change	d	0.62	0.21	2.99	0.003	0.38	0.12	3.20	0.001
North-East	beta-xylosidase	pH	Xylosidase	~	LUI_historic	e	0.07	0.10	0.77	0.441	0.11	0.14	0.77	0.440
North-East	beta-xylosidase	pH	Xylosidase	~	LUI_change	f	0.32	0.16	1.95	0.052	0.27	0.14	1.99	0.046
North-East	beta-xylosidase	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	beta-xylosidase	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	beta-xylosidase	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	beta-xylosidase	pH	Xylosidase	~~	Xylosidase		0.03	0.01	5.00	0.000	0.79	0.10	7.67	0.000
North-East	beta-xylosidase	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	beta-xylosidase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.13	0.899	0.00	0.01	-0.13	0.899
North-East	beta-xylosidase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.03	0.06	0.40	0.689	0.02	0.05	0.40	0.687
North-East	beta-xylosidase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.10	0.76	0.448	0.11	0.14	0.76	0.447
North-East	beta-xylosidase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.34	0.17	1.96	0.049	0.29	0.14	2.03	0.042
North-East	beta-xylosidase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.07	0.10	0.69	0.488	-0.02	0.13	-0.15	0.879
North-East	beta-xylosidase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.34	0.17	1.97	0.049	0.25	0.13	1.86	0.063
North-East	chitinase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	chitinase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	chitinase	CWM_leaf_P	Chitinase	~	CWM_leafP_historic	c	0.26	0.12	2.23	0.025	0.29	0.12	2.32	0.020
North-East	chitinase	CWM_leaf_P	Chitinase	~	CWM_leafP_change	d	0.21	0.12	1.75	0.081	0.23	0.13	1.78	0.075
North-East	chitinase	CWM_leaf_P	Chitinase	~	LUI_historic	e	0.04	0.10	0.39	0.699	0.06	0.14	0.39	0.699
North-East	chitinase	CWM_leaf_P	Chitinase	~	LUI_change	f	0.32	0.17	1.92	0.055	0.28	0.14	1.97	0.049
North-East	chitinase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	chitinase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	chitinase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	chitinase	CWM_leaf_P	Chitinase	~~	Chitinase		0.03	0.01	5.00	0.000	0.83	0.10	8.66	0.000
North-East	chitinase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	chitinase	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	chitinase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.03	0.32	0.749	0.01	0.04	0.32	0.749
North-East	chitinase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.06	0.05	-1.24	0.214	-0.06	0.05	-1.25	0.212
North-East	chitinase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.10	0.46	0.645	0.07	0.15	0.46	0.645
North-East	chitinase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.26	0.17	1.53	0.125	0.22	0.14	1.56	0.118
North-East	chitinase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.04	0.10	0.41	0.680	-0.03	0.14	-0.20	0.839
North-East	chitinase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.25	0.17	1.54	0.125	0.19	0.13	1.48	0.139
North-East	chitinase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	chitinase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	chitinase	CWM_MycInt	Chitinase	~	CWM_MycInt_historic	c	0.12	0.14	0.92	0.359	0.13	0.14	0.92	0.356
North-East	chitinase	CWM_MycInt	Chitinase	~	CWM_MycInt_change	d	-0.09	0.14	-0.67	0.506	-0.09	0.14	-0.67	0.504
North-East	chitinase	CWM_MycInt	Chitinase	~	LUI_historic	e	0.01	0.10	0.08	0.933	0.01	0.15	0.08	0.933
North-East	chitinase	CWM_MycInt	Chitinase	~	LUI_change	f	0.25	0.17	1.51	0.130	0.23	0.15	1.55	0.122
North-East	chitinase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	chitinase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	chitinase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.94	0.000
North-East	chitinase	CWM_MycInt	Chitinase	~~	Chitinase		0.03	0.01	5.00	0.000	0.92	0.07	12.94	0.000
North-East	chitinase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	chitinase	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	chitinase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.02	0.81	0.419	0.03	0.04	0.81	0.416
North-East	chitinase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.03	0.56	0.578	0.01	0.02	0.56	0.577
North-East	chitinase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.03	0.10	0.29	0.775	0.04	0.15	0.29	0.775
North-East	chitinase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.27	0.17	1.61	0.108	0.24	0.15	1.65	0.100
North-East	chitinase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.02	0.10	0.23	0.817	-0.06	0.14	-0.44	0.662
North-East	chitinase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.26	0.16	1.61	0.107	0.22	0.13	1.68	0.093

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
North-East	chitinase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	chitinase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	chitinase	Plant_biomass	Chitinase	~	Plant_biomass	c	-0.05	0.12	-0.44	0.660	-0.06	0.14	-0.44	0.660
North-East	chitinase	Plant_biomass	Chitinase	~	LUI_historic	e	0.07	0.10	0.68	0.499	0.11	0.16	0.68	0.498
North-East	chitinase	Plant_biomass	Chitinase	~	LUI_change	f	0.33	0.17	1.96	0.050	0.30	0.15	2.04	0.042
North-East	chitinase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	chitinase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	chitinase	Plant_biomass	Chitinase	~~	Chitinase		0.03	0.01	4.95	0.000	0.92	0.07	12.63	0.000
North-East	chitinase	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	chitinase	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	chitinase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.02	-0.42	0.672	-0.02	0.04	-0.42	0.671
North-East	chitinase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	-0.17	0.862	0.00	0.01	-0.17	0.862
North-East	chitinase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.10	0.59	0.554	0.09	0.15	0.59	0.553
North-East	chitinase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.33	0.17	1.95	0.052	0.30	0.15	2.02	0.043
North-East	chitinase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.05	0.10	0.53	0.597	-0.04	0.14	-0.27	0.791
North-East	chitinase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.33	0.17	1.95	0.051	0.26	0.13	1.93	0.053
North-East	chitinase	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	chitinase	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	chitinase	Lignin_content	Chitinase	~	Lignin_content	c	0.04	0.12	0.36	0.718	0.05	0.14	0.36	0.718
North-East	chitinase	Lignin_content	Chitinase	~	LUI_historic	e	0.05	0.10	0.48	0.632	0.08	0.16	0.48	0.631
North-East	chitinase	Lignin_content	Chitinase	~	LUI_change	f	0.32	0.17	1.87	0.062	0.29	0.15	1.93	0.053
North-East	chitinase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	chitinase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	chitinase	Lignin_content	Chitinase	~~	Chitinase		0.03	0.01	4.95	0.000	0.92	0.07	12.73	0.000
North-East	chitinase	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	chitinase	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	chitinase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.03	0.36	0.723	0.02	0.04	0.36	0.723
North-East	chitinase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.03	0.34	0.731	0.01	0.03	0.34	0.731
North-East	chitinase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.10	0.59	0.554	0.09	0.15	0.59	0.553
North-East	chitinase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.33	0.17	1.95	0.052	0.30	0.15	2.02	0.043
North-East	chitinase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.05	0.10	0.53	0.597	-0.04	0.14	-0.27	0.791
North-East	chitinase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.33	0.17	1.95	0.051	0.26	0.13	1.93	0.053
North-East	chitinase	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	chitinase	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	chitinase	pH	Chitinase	~	pH_historic	c	0.03	0.08	0.35	0.727	0.05	0.13	0.35	0.726
North-East	chitinase	pH	Chitinase	~	pH_change	d	0.49	0.20	2.38	0.017	0.31	0.12	2.48	0.013
North-East	chitinase	pH	Chitinase	~	LUI_historic	e	0.09	0.09	0.92	0.356	0.13	0.14	0.93	0.354
North-East	chitinase	pH	Chitinase	~	LUI_change	f	0.33	0.16	2.08	0.038	0.30	0.14	2.15	0.032
North-East	chitinase	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	chitinase	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	chitinase	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	chitinase	pH	Chitinase	~~	Chitinase		0.03	0.01	5.00	0.000	0.83	0.10	8.48	0.000
North-East	chitinase	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	chitinase	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	chitinase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	-0.12	0.903	0.00	0.01	-0.12	0.903
North-East	chitinase	pH	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.05	0.40	0.691	0.02	0.04	0.40	0.689
North-East	chitinase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.09	0.09	0.92	0.360	0.13	0.14	0.92	0.357
North-East	chitinase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.35	0.17	2.11	0.035	0.31	0.14	2.20	0.028
North-East	chitinase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.08	0.09	0.85	0.395	-0.01	0.14	-0.03	0.973
North-East	chitinase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.35	0.17	2.11	0.035	0.26	0.13	1.95	0.051
North-East	urease	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	urease	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	urease	CWM_leaf_P	Urease	~	CWM_leafP_historic	c	0.10	0.12	0.84	0.400	0.12	0.14	0.85	0.397
North-East	urease	CWM_leaf_P	Urease	~	CWM_leafP_change	d	0.00	0.12	-0.03	0.976	0.00	0.14	-0.03	0.976
North-East	urease	CWM_leaf_P	Urease	~	LUI_historic	e	0.07	0.10	0.73	0.463	0.11	0.15	0.74	0.461
North-East	urease	CWM_leaf_P	Urease	~	LUI_change	f	-0.06	0.17	-0.37	0.711	-0.06	0.16	-0.37	0.711
North-East	urease	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	urease	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	urease	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	urease	CWM_leaf_P	Urease	~~	Urease		0.03	0.01	5.00	0.000	0.96	0.05	18.45	0.000
North-East	urease	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	urease	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	urease	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.30	0.763	0.01	0.02	0.30	0.763
North-East	urease	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.04	0.03	0.976	0.00	0.04	0.03	0.976
North-East	urease	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.10	0.77	0.444	0.12	0.15	0.77	0.442
North-East	urease	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.06	0.16	-0.37	0.710	-0.06	0.15	-0.37	0.709
North-East	urease	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.08	0.10	0.79	0.430	0.14	0.14	1.03	0.302
North-East	urease	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.06	0.16	-0.38	0.701	-0.11	0.14	-0.78	0.436

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P*.std
North-East	urease	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	urease	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	urease	CWM_MycInt	Urease	~	CWM_MycInt_historic	c	0.02	0.13	0.17	0.867	0.02	0.14	0.17	0.867
North-East	urease	CWM_MycInt	Urease	~	CWM_MycInt_change	d	-0.25	0.14	-1.83	0.068	-0.25	0.13	-1.88	0.060
North-East	urease	CWM_MycInt	Urease	~	LUI_historic	e	0.03	0.10	0.26	0.792	0.04	0.15	0.26	0.792
North-East	urease	CWM_MycInt	Urease	~	LUI_change	f	-0.12	0.16	-0.72	0.472	-0.11	0.15	-0.72	0.470
North-East	urease	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	urease	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	urease	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	urease	CWM_MycInt	Urease	~~	Urease		0.03	0.01	5.00	0.000	0.93	0.07	13.11	0.000
North-East	urease	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	urease	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	urease	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.17	0.867	0.01	0.03	0.17	0.867
North-East	urease	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.04	0.04	0.89	0.376	0.04	0.04	0.89	0.374
North-East	urease	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.03	0.09	0.31	0.760	0.05	0.15	0.31	0.759
North-East	urease	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.08	0.16	-0.48	0.633	-0.07	0.16	-0.48	0.633
North-East	urease	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.03	0.09	0.33	0.743	0.08	0.14	0.57	0.569
North-East	urease	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.08	0.16	-0.48	0.629	-0.09	0.14	-0.67	0.503
North-East	urease	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	urease	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	urease	Plant_biomass	Urease	~	Plant_biomass	c	0.04	0.12	0.32	0.748	0.05	0.15	0.32	0.748
North-East	urease	Plant_biomass	Urease	~	LUI_historic	e	0.07	0.10	0.74	0.458	0.12	0.16	0.75	0.455
North-East	urease	Plant_biomass	Urease	~	LUI_change	f	-0.03	0.17	-0.19	0.852	-0.03	0.16	-0.19	0.852
North-East	urease	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	urease	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	urease	Plant_biomass	Urease	~~	Urease		0.03	0.01	4.95	0.000	0.98	0.04	23.05	0.000
North-East	urease	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	urease	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	urease	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.32	0.753	0.01	0.04	0.32	0.753
North-East	urease	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.16	0.871	0.00	0.01	0.16	0.871
North-East	urease	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.08	0.10	0.84	0.404	0.13	0.16	0.84	0.400
North-East	urease	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.03	0.17	-0.18	0.859	-0.03	0.16	-0.18	0.859
North-East	urease	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.08	0.10	0.85	0.393	0.14	0.14	1.02	0.308
North-East	urease	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.03	0.16	-0.19	0.850	-0.08	0.14	-0.59	0.553
North-East	urease	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	urease	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	urease	Lignin_content	Urease	~	Lignin_content	c	0.04	0.12	0.31	0.757	0.05	0.15	0.31	0.757
North-East	urease	Lignin_content	Urease	~	LUI_historic	e	0.07	0.10	0.73	0.467	0.12	0.16	0.73	0.464
North-East	urease	Lignin_content	Urease	~	LUI_change	f	-0.04	0.17	-0.22	0.823	-0.04	0.16	-0.22	0.823
North-East	urease	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	urease	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	urease	Lignin_content	Urease	~~	Urease		0.03	0.01	4.95	0.000	0.98	0.04	23.12	0.000
North-East	urease	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	urease	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	urease	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.03	0.31	0.760	0.01	0.04	0.31	0.760
North-East	urease	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.03	0.30	0.765	0.01	0.03	0.30	0.765
North-East	urease	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.08	0.10	0.84	0.404	0.13	0.16	0.84	0.400
North-East	urease	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	-0.03	0.17	-0.18	0.859	-0.03	0.16	-0.18	0.859
North-East	urease	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.08	0.10	0.85	0.393	0.14	0.14	1.02	0.308
North-East	urease	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	-0.03	0.16	-0.19	0.850	-0.08	0.14	-0.59	0.553
North-East	urease	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	urease	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	urease	pH	Urease	~	pH_historic	c	0.27	0.06	4.19	0.000	0.42	0.10	4.38	0.000
North-East	urease	pH	Urease	~	pH_change	d	0.90	0.17	5.34	0.000	0.54	0.09	5.96	0.000
North-East	urease	pH	Urease	~	LUI_historic	e	0.16	0.08	2.03	0.042	0.23	0.11	2.04	0.041
North-East	urease	pH	Urease	~	LUI_change	f	0.06	0.13	0.45	0.652	0.05	0.11	0.45	0.652
North-East	urease	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	urease	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	urease	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	urease	pH	Urease	~~	Urease		0.02	0.00	5.00	0.000	0.50	0.09	5.34	0.000
North-East	urease	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	urease	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	urease	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.04	-0.13	0.897	-0.01	0.06	-0.13	0.897
North-East	urease	pH	LUI_change_in	:=	b*d	LUI_change_in	0.04	0.09	0.40	0.687	0.03	0.08	0.40	0.687
North-East	urease	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.15	0.09	1.73	0.084	0.22	0.12	1.75	0.080
North-East	urease	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.10	0.16	0.60	0.548	0.08	0.13	0.60	0.548
North-East	urease	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.15	0.09	1.73	0.084	0.18	0.12	1.52	0.127
North-East	urease	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.09	0.16	0.58	0.560	-0.01	0.13	-0.10	0.920

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P*.std
North-East	DEA	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	DEA	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	DEA	CWM_leaf_P	DEA	~	CWM_leafP_historic	c	0.41	0.15	2.81	0.005	0.37	0.12	3.02	0.003
North-East	DEA	CWM_leaf_P	DEA	~	CWM_leafP_change	d	0.13	0.15	0.88	0.379	0.12	0.13	0.88	0.377
North-East	DEA	CWM_leaf_P	DEA	~	LUI_historic	e	-0.06	0.12	-0.54	0.591	-0.08	0.14	-0.54	0.591
North-East	DEA	CWM_leaf_P	DEA	~	LUI_change	f	-0.04	0.21	-0.19	0.850	-0.03	0.15	-0.19	0.850
North-East	DEA	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	DEA	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	DEA	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	DEA	CWM_leaf_P	DEA	~~	DEA		0.05	0.01	5.00	0.000	0.85	0.09	9.16	0.000
North-East	DEA	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	DEA	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	DEA	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.04	0.32	0.748	0.02	0.05	0.32	0.748
North-East	DEA	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.04	0.05	-0.79	0.431	-0.03	0.04	-0.79	0.429
North-East	DEA	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.05	0.13	-0.40	0.692	-0.06	0.15	-0.40	0.691
North-East	DEA	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	-0.08	0.20	-0.39	0.697	-0.06	0.15	-0.39	0.696
North-East	DEA	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.05	0.12	-0.39	0.697	-0.04	0.14	-0.26	0.795
North-East	DEA	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	-0.08	0.20	-0.39	0.699	-0.03	0.13	-0.23	0.820
North-East	DEA	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	DEA	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	DEA	CWM_MycInt	DEA	~	CWM_MycInt_historic	c	-0.34	0.16	-2.15	0.032	-0.26	0.12	-2.20	0.028
North-East	DEA	CWM_MycInt	DEA	~	CWM_MycInt_change	d	-0.65	0.16	-3.97	0.000	-0.47	0.11	-4.44	0.000
North-East	DEA	CWM_MycInt	DEA	~	LUI_historic	e	-0.07	0.12	-0.63	0.528	-0.08	0.13	-0.63	0.527
North-East	DEA	CWM_MycInt	DEA	~	LUI_change	f	-0.04	0.19	-0.22	0.825	-0.03	0.13	-0.22	0.825
North-East	DEA	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	DEA	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	DEA	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	DEA	CWM_MycInt	DEA	~~	DEA		0.04	0.01	5.00	0.000	0.69	0.11	6.55	0.000
North-East	DEA	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	DEA	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	DEA	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.05	0.04	-1.34	0.180	-0.06	0.05	-1.36	0.174
North-East	DEA	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.10	0.10	0.98	0.326	0.07	0.07	0.99	0.321
North-East	DEA	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.13	0.12	-1.08	0.281	-0.15	0.13	-1.08	0.278
North-East	DEA	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.06	0.22	0.26	0.795	0.04	0.15	0.26	0.795
North-East	DEA	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	-0.13	0.12	-1.10	0.270	-0.16	0.13	-1.30	0.195
North-East	DEA	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.06	0.22	0.27	0.785	0.10	0.14	0.74	0.461
North-East	DEA	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	DEA	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	DEA	Plant_biomass	DEA	~	Plant_biomass	c	-0.09	0.15	-0.59	0.555	-0.09	0.15	-0.59	0.553
North-East	DEA	Plant_biomass	DEA	~	LUI_historic	e	-0.01	0.13	-0.05	0.957	-0.01	0.16	-0.05	0.957
North-East	DEA	Plant_biomass	DEA	~	LUI_change	f	0.05	0.21	0.22	0.824	0.04	0.16	0.22	0.824
North-East	DEA	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	DEA	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	DEA	Plant_biomass	DEA	~~	DEA		0.05	0.01	4.95	0.000	0.99	0.03	35.23	0.000
North-East	DEA	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	DEA	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	DEA	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.03	-0.56	0.579	-0.02	0.04	-0.56	0.578
North-East	DEA	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.02	-0.18	0.857	0.00	0.01	-0.18	0.857
North-East	DEA	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.02	0.12	-0.19	0.849	-0.03	0.16	-0.19	0.849
North-East	DEA	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.04	0.21	0.21	0.837	0.03	0.16	0.21	0.836
North-East	DEA	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.03	0.12	-0.20	0.841	-0.04	0.14	-0.31	0.757
North-East	DEA	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.04	0.21	0.21	0.834	0.05	0.14	0.32	0.749
North-East	DEA	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	DEA	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	DEA	Lignin_content	DEA	~	Lignin_content	c	-0.06	0.15	-0.38	0.702	-0.06	0.15	-0.38	0.702
North-East	DEA	Lignin_content	DEA	~	LUI_historic	e	-0.01	0.13	-0.09	0.932	-0.01	0.16	-0.09	0.932
North-East	DEA	Lignin_content	DEA	~	LUI_change	f	0.06	0.21	0.26	0.792	0.04	0.16	0.26	0.792
North-East	DEA	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	DEA	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	DEA	Lignin_content	DEA	~~	DEA		0.05	0.01	4.95	0.000	0.99	0.02	46.04	0.000
North-East	DEA	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	DEA	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	DEA	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.38	0.708	-0.02	0.04	-0.38	0.708
North-East	DEA	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	-0.01	0.04	-0.36	0.718	-0.01	0.03	-0.36	0.717
North-East	DEA	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	-0.02	0.12	-0.19	0.849	-0.03	0.16	-0.19	0.849
North-East	DEA	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.04	0.21	0.21	0.837	0.03	0.16	0.21	0.836
North-East	DEA	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	-0.03	0.12	-0.20	0.841	-0.04	0.14	-0.31	0.757
North-East	DEA	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.04	0.21	0.21	0.834	0.05	0.14	0.32	0.749

Table S6.2 continued

Region	**MO variable**	**mediator**	**lhs**	**op**	**rhs**	**label**	**est**	**se**	**z**	***P***	**est.std**	**se.std**	**z.std**	***P*.std**
North-East	DEA	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	DEA	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	DEA	pH	DEA	~	pH_historic	c	0.50	0.08	6.27	0.000	0.62	0.08	7.55	0.000
North-East	DEA	pH	DEA	~	pH_change	d	0.75	0.21	3.55	0.000	0.35	0.10	3.62	0.000
North-East	DEA	pH	DEA	~	LUI_historic	e	0.07	0.10	0.71	0.476	0.08	0.11	0.71	0.476
North-East	DEA	pH	DEA	~	LUI_change	f	0.21	0.16	1.25	0.212	0.14	0.11	1.25	0.211
North-East	DEA	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	DEA	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	DEA	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	DEA	pH	DEA	~~	DEA		0.03	0.01	5.00	0.000	0.48	0.09	5.18	0.000
North-East	DEA	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	DEA	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	DEA	pH	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.08	-0.13	0.897	-0.01	0.09	-0.13	0.897
North-East	DEA	pH	LUI_change_in	:=	b*d	LUI_change_in	0.03	0.08	0.40	0.688	0.02	0.05	0.40	0.688
North-East	DEA	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.12	0.48	0.634	0.07	0.14	0.48	0.634
North-East	DEA	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.24	0.18	1.31	0.192	0.16	0.12	1.31	0.190
North-East	DEA	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.12	0.44	0.660	0.00	0.13	-0.01	0.994
North-East	DEA	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.23	0.18	1.31	0.192	0.13	0.12	1.10	0.272
North-East	phosphatase	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	phosphatase	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	phosphatase	CWM_leaf_P	Phosphatase	~	CWM_leafP_historic	c	-0.19	0.08	-2.31	0.021	-0.28	0.12	-2.39	0.017
North-East	phosphatase	CWM_leaf_P	Phosphatase	~	CWM_leafP_change	d	0.04	0.08	0.47	0.640	0.06	0.13	0.47	0.640
North-East	phosphatase	CWM_leaf_P	Phosphatase	~	LUI_historic	e	0.12	0.07	1.80	0.072	0.24	0.13	1.83	0.067
North-East	phosphatase	CWM_leaf_P	Phosphatase	~	LUI_change	f	0.38	0.11	3.36	0.001	0.47	0.13	3.63	0.000
North-East	phosphatase	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	phosphatase	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	phosphatase	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	phosphatase	CWM_leaf_P	Phosphatase	~~	Phosphatase		0.02	0.00	5.00	0.000	0.75	0.10	7.25	0.000
North-East	phosphatase	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	phosphatase	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	phosphatase	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.02	-0.32	0.749	-0.01	0.04	-0.32	0.749
North-East	phosphatase	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.03	-0.45	0.651	-0.01	0.03	-0.45	0.651
North-East	phosphatase	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.11	0.07	1.64	0.102	0.23	0.14	1.66	0.097
North-East	phosphatase	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.37	0.11	3.33	0.001	0.45	0.13	3.60	0.000
North-East	phosphatase	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.11	0.07	1.54	0.123	0.04	0.14	0.26	0.796
North-East	phosphatase	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.37	0.11	3.33	0.001	0.35	0.12	2.94	0.003
North-East	phosphatase	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	phosphatase	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	phosphatase	CWM_MycInt	Phosphatase	~	CWM_MycInt_historic	c	-0.13	0.10	-1.39	0.166	-0.18	0.13	-1.40	0.161
North-East	phosphatase	CWM_MycInt	Phosphatase	~	CWM_MycInt_change	d	-0.09	0.10	-0.94	0.349	-0.12	0.13	-0.94	0.346
North-East	phosphatase	CWM_MycInt	Phosphatase	~	LUI_historic	e	0.11	0.07	1.58	0.114	0.23	0.14	1.61	0.108
North-East	phosphatase	CWM_MycInt	Phosphatase	~	LUI_change	f	0.34	0.12	2.87	0.004	0.41	0.13	3.06	0.002
North-East	phosphatase	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	phosphatase	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	phosphatase	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	phosphatase	CWM_MycInt	Phosphatase	~~	Phosphatase		0.02	0.00	5.00	0.000	0.81	0.10	8.19	0.000
North-East	phosphatase	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	phosphatase	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	phosphatase	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.02	-1.08	0.281	-0.04	0.04	-1.09	0.278
North-East	phosphatase	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.01	0.02	0.69	0.492	0.02	0.03	0.69	0.489
North-East	phosphatase	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.09	0.07	1.30	0.195	0.19	0.14	1.31	0.191
North-East	phosphatase	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.35	0.12	2.99	0.003	0.42	0.13	3.22	0.001
North-East	phosphatase	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.08	0.07	1.21	0.228	0.00	0.14	0.02	0.986
North-East	phosphatase	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.35	0.12	2.99	0.003	0.35	0.12	2.80	0.005
North-East	phosphatase	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	phosphatase	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	phosphatase	Plant_biomass	Phosphatase	~	Plant_biomass	c	0.02	0.09	0.22	0.824	0.03	0.14	0.22	0.824
North-East	phosphatase	Plant_biomass	Phosphatase	~	LUI_historic	e	0.09	0.07	1.30	0.194	0.20	0.15	1.32	0.188
North-East	phosphatase	Plant_biomass	Phosphatase	~	LUI_change	f	0.32	0.12	2.64	0.008	0.39	0.14	2.81	0.005
North-East	phosphatase	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	phosphatase	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	phosphatase	Plant_biomass	Phosphatase	~~	Phosphatase		0.02	0.00	4.95	0.000	0.87	0.09	9.82	0.000
North-East	phosphatase	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	phosphatase	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	phosphatase	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.22	0.826	0.01	0.03	0.22	0.826
North-East	phosphatase	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.01	0.14	0.886	0.00	0.01	0.14	0.886
North-East	phosphatase	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.10	0.07	1.38	0.167	0.21	0.15	1.40	0.161
North-East	phosphatase	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.32	0.12	2.65	0.008	0.39	0.14	2.82	0.005
North-East	phosphatase	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.09	0.07	1.31	0.192	0.04	0.14	0.25	0.801
North-East	phosphatase	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.32	0.12	2.64	0.008	0.30	0.13	2.34	0.019

Table S6.2 continued

Region	**MO variable**	**mediator**	**lhs**	**op**	**rhs**	**label**	**est**	**se**	**z**	***P***	**est.std**	**se.std**	**z.std**	***P* .std**
North-East	phosphatase	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	phosphatase	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	phosphatase	Lignin_content	Phosphatase	~	Lignin_content	c	0.01	0.09	0.09	0.926	0.01	0.14	0.09	0.926
North-East	phosphatase	Lignin_content	Phosphatase	~	LUI_historic	e	0.10	0.07	1.31	0.189	0.20	0.15	1.33	0.184
North-East	phosphatase	Lignin_content	Phosphatase	~	LUI_change	f	0.32	0.12	2.60	0.009	0.39	0.14	2.76	0.006
North-East	phosphatase	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	phosphatase	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	phosphatase	Lignin_content	Phosphatase	~~	Phosphatase		0.02	0.00	4.95	0.000	0.87	0.09	9.85	0.000
North-East	phosphatase	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	phosphatase	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	phosphatase	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.09	0.926	0.00	0.04	0.09	0.926
North-East	phosphatase	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.02	0.09	0.927	0.00	0.02	0.09	0.927
North-East	phosphatase	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.10	0.07	1.38	0.167	0.21	0.15	1.40	0.161
North-East	phosphatase	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.32	0.12	2.65	0.008	0.39	0.14	2.82	0.005
North-East	phosphatase	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.09	0.07	1.31	0.192	0.04	0.14	0.25	0.801
North-East	phosphatase	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.32	0.12	2.64	0.008	0.30	0.13	2.34	0.019
North-East	phosphatase	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	phosphatase	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	phosphatase	pH	Phosphatase	~	pH_historic	c	-0.11	0.05	-2.00	0.046	-0.25	0.12	-2.05	0.041
North-East	phosphatase	pH	Phosphatase	~	pH_change	d	-0.38	0.14	-2.61	0.009	-0.32	0.12	-2.73	0.006
North-East	phosphatase	pH	Phosphatase	~	LUI_historic	e	0.07	0.07	1.01	0.315	0.14	0.14	1.01	0.312
North-East	phosphatase	pH	Phosphatase	~	LUI_change	f	0.28	0.11	2.52	0.012	0.34	0.13	2.62	0.009
North-East	phosphatase	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	phosphatase	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	phosphatase	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	phosphatase	pH	Phosphatase	~~	Phosphatase		0.02	0.00	5.00	0.000	0.75	0.10	7.29	0.000
North-East	phosphatase	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	phosphatase	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	phosphatase	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.13	0.897	0.00	0.04	0.13	0.897
North-East	phosphatase	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.04	-0.40	0.690	-0.02	0.05	-0.40	0.691
North-East	phosphatase	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.07	1.01	0.314	0.14	0.14	1.01	0.312
North-East	phosphatase	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.27	0.12	2.27	0.023	0.33	0.14	2.36	0.018
North-East	phosphatase	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.06	0.07	0.94	0.349	0.00	0.14	0.01	0.993
North-East	phosphatase	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.12	2.27	0.023	0.26	0.13	2.06	0.040
North-East	bacteria	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	bacteria	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	bacteria	CWM_leaf_P	bactotal	~	CWM_leafP_historic	c	0.23	0.12	2.01	0.045	0.26	0.13	2.07	0.038
North-East	bacteria	CWM_leaf_P	bactotal	~	CWM_leafP_change	d	0.16	0.12	1.32	0.186	0.18	0.13	1.34	0.181
North-East	bacteria	CWM_leaf_P	bactotal	~	LUI_historic	e	0.00	0.09	0.03	0.975	0.01	0.15	0.03	0.975
North-East	bacteria	CWM_leaf_P	bactotal	~	LUI_change	f	0.25	0.16	1.56	0.120	0.23	0.15	1.58	0.113
North-East	bacteria	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	bacteria	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	bacteria	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	bacteria	CWM_leaf_P	bactotal	~~	bactotal		0.03	0.01	5.00	0.000	0.87	0.09	9.84	0.000
North-East	bacteria	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	bacteria	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	bacteria	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.32	0.750	0.01	0.04	0.32	0.750
North-East	bacteria	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.05	0.05	-1.06	0.290	-0.04	0.04	-1.07	0.287
North-East	bacteria	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.01	0.10	0.11	0.912	0.02	0.15	0.11	0.912
North-East	bacteria	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.21	0.16	1.28	0.201	0.19	0.15	1.30	0.195
North-East	bacteria	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.01	0.10	0.07	0.947	-0.07	0.14	-0.47	0.641
North-East	bacteria	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.21	0.16	1.28	0.200	0.18	0.13	1.37	0.171
North-East	bacteria	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	bacteria	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	bacteria	CWM_MycInt	bactotal	~	CWM_MycInt_historic	c	0.46	0.12	3.75	0.000	0.45	0.11	4.10	0.000
North-East	bacteria	CWM_MycInt	bactotal	~	CWM_MycInt_change	d	0.36	0.13	2.79	0.005	0.33	0.11	2.90	0.004
North-East	bacteria	CWM_MycInt	bactotal	~	LUI_historic	e	-0.02	0.09	-0.22	0.827	-0.03	0.13	-0.22	0.827
North-East	bacteria	CWM_MycInt	bactotal	~	LUI_change	f	0.21	0.15	1.38	0.169	0.18	0.13	1.39	0.166
North-East	bacteria	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	bacteria	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	bacteria	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.94	0.000
North-East	bacteria	CWM_MycInt	bactotal	~~	bactotal		0.03	0.01	5.00	0.000	0.69	0.11	6.56	0.000
North-East	bacteria	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	bacteria	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	bacteria	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.07	0.05	1.56	0.119	0.11	0.07	1.58	0.115
North-East	bacteria	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.05	0.06	-0.95	0.341	-0.05	0.05	-0.95	0.341
North-East	bacteria	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.10	0.54	0.590	0.08	0.14	0.54	0.590
North-East	bacteria	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.15	0.16	0.97	0.333	0.13	0.14	0.97	0.331
North-East	bacteria	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.10	0.51	0.609	0.02	0.14	0.15	0.882
North-East	bacteria	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.15	0.16	0.97	0.334	0.10	0.13	0.78	0.437

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
North-East	bacteria	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	bacteria	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	bacteria	Plant_biomass	bactotal	~	Plant_biomass	c	0.19	0.11	1.65	0.099	0.23	0.14	1.69	0.092
North-East	bacteria	Plant_biomass	bactotal	~	LUI_historic	e	-0.01	0.10	-0.14	0.888	-0.02	0.15	-0.14	0.888
North-East	bacteria	Plant_biomass	bactotal	~	LUI_change	f	0.26	0.16	1.61	0.108	0.24	0.15	1.65	0.100
North-East	bacteria	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	bacteria	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	bacteria	Plant_biomass	bactotal	~~	bactotal		0.03	0.01	4.95	0.000	0.90	0.08	10.81	0.000
North-East	bacteria	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	bacteria	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	bacteria	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.04	0.03	1.15	0.250	0.06	0.05	1.16	0.245
North-East	bacteria	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.04	0.19	0.851	0.01	0.04	0.19	0.851
North-East	bacteria	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.02	0.10	0.23	0.820	0.04	0.15	0.23	0.820
North-East	bacteria	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.27	0.17	1.61	0.107	0.25	0.15	1.65	0.099
North-East	bacteria	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.02	0.10	0.17	0.863	-0.07	0.14	-0.50	0.614
North-East	bacteria	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.16	1.62	0.106	0.23	0.14	1.72	0.085
North-East	bacteria	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	bacteria	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	bacteria	Lignin_content	bactotal	~	Lignin_content	c	0.00	0.12	-0.04	0.970	-0.01	0.14	-0.04	0.970
North-East	bacteria	Lignin_content	bactotal	~	LUI_historic	e	0.02	0.10	0.23	0.818	0.04	0.16	0.23	0.818
North-East	bacteria	Lignin_content	bactotal	~	LUI_change	f	0.27	0.17	1.60	0.111	0.25	0.15	1.64	0.102
North-East	bacteria	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	bacteria	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	bacteria	Lignin_content	bactotal	~~	bactotal		0.03	0.01	4.95	0.000	0.95	0.06	14.90	0.000
North-East	bacteria	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	bacteria	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	bacteria	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.03	-0.04	0.970	0.00	0.04	-0.04	0.970
North-East	bacteria	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.03	-0.04	0.970	0.00	0.03	-0.04	0.970
North-East	bacteria	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.02	0.10	0.23	0.820	0.04	0.15	0.23	0.820
North-East	bacteria	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.27	0.17	1.61	0.107	0.25	0.15	1.65	0.099
North-East	bacteria	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.02	0.10	0.17	0.863	-0.07	0.14	-0.50	0.614
North-East	bacteria	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.16	1.62	0.106	0.23	0.14	1.72	0.085
North-East	bacteria	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	bacteria	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	bacteria	pH	bactotal	~	pH_historic	c	0.01	0.08	0.08	0.938	0.01	0.14	0.08	0.938
North-East	bacteria	pH	bactotal	~	pH_change	d	0.09	0.21	0.42	0.678	0.06	0.14	0.42	0.678
North-East	bacteria	pH	bactotal	~	LUI_historic	e	0.03	0.10	0.29	0.774	0.04	0.15	0.29	0.774
North-East	bacteria	pH	bactotal	~	LUI_change	f	0.27	0.16	1.65	0.099	0.25	0.15	1.69	0.090
North-East	bacteria	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	bacteria	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	bacteria	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	bacteria	pH	bactotal	~~	bactotal		0.03	0.01	5.00	0.000	0.94	0.07	14.39	0.000
North-East	bacteria	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	bacteria	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	bacteria	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	-0.07	0.947	0.00	0.00	-0.07	0.947
North-East	bacteria	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	0.29	0.772	0.00	0.01	0.29	0.772
North-East	bacteria	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.03	0.10	0.29	0.775	0.04	0.15	0.29	0.775
North-East	bacteria	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.27	0.16	1.67	0.095	0.25	0.15	1.72	0.086
North-East	bacteria	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.02	0.10	0.23	0.818	-0.07	0.14	-0.47	0.638
North-East	bacteria	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.27	0.16	1.68	0.094	0.24	0.13	1.76	0.078
North-East	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	CWM_leafP_historic	c	-0.24	0.11	-2.31	0.021	-0.29	0.12	-2.40	0.016
North-East	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	CWM_leafP_change	d	-0.26	0.11	-2.41	0.016	-0.31	0.12	-2.52	0.012
North-East	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	LUI_historic	e	0.06	0.09	0.69	0.487	0.10	0.14	0.70	0.486
North-East	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~	LUI_change	f	0.13	0.15	0.86	0.390	0.12	0.14	0.86	0.388
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	fungi:bacteria ratio	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	fungi:bacteria ratio	CWM_leaf_P	fungi_bac	~~	fungi_bac		0.03	0.01	5.00	0.000	0.79	0.10	7.95	0.000
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	-0.01	0.03	-0.32	0.749	-0.01	0.04	-0.32	0.749
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.08	0.06	1.43	0.154	0.08	0.05	1.46	0.145
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.09	0.58	0.565	0.08	0.15	0.58	0.564
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.21	0.15	1.36	0.173	0.20	0.14	1.38	0.167
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.09	0.53	0.593	0.00	0.14	-0.01	0.989
North-East	fungi:bacteria ratio	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.21	0.15	1.36	0.173	0.16	0.13	1.22	0.221

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
North-East	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	CWM_MycInt_historic	c	-0.19	0.12	-1.56	0.120	-0.22	0.14	-1.59	0.112
North-East	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	CWM_MycInt_change	d	-0.02	0.13	-0.17	0.869	-0.02	0.14	-0.17	0.869
North-East	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	LUI_historic	e	0.09	0.09	0.95	0.343	0.15	0.15	0.96	0.339
North-East	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~	LUI_change	f	0.21	0.15	1.39	0.166	0.21	0.15	1.41	0.159
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	fungi:bacteria ratio	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.94	0.000
North-East	fungi:bacteria ratio	CWM_MycInt	fungi_bac	~~	fungi_bac		0.03	0.01	5.00	0.000	0.92	0.07	12.48	0.000
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	-0.03	0.03	-1.15	0.249	-0.05	0.04	-1.17	0.244
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.02	0.16	0.871	0.00	0.02	0.16	0.871
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.09	0.62	0.537	0.10	0.15	0.62	0.535
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.21	0.15	1.42	0.156	0.21	0.15	1.44	0.149
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.09	0.58	0.564	0.00	0.14	0.02	0.984
North-East	fungi:bacteria ratio	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.21	0.15	1.42	0.156	0.17	0.14	1.28	0.201
North-East	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	Plant_biomass	c	-0.08	0.10	-0.81	0.415	-0.12	0.14	-0.82	0.412
North-East	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	LUI_historic	e	0.06	0.09	0.70	0.486	0.11	0.16	0.70	0.484
North-East	fungi:bacteria ratio	Plant_biomass	fungi_bac	~	LUI_change	f	0.17	0.14	1.17	0.241	0.18	0.15	1.19	0.234
North-East	fungi:bacteria ratio	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	fungi:bacteria ratio	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	fungi:bacteria ratio	Plant_biomass	fungi_bac	~~	fungi_bac		0.02	0.01	4.95	0.000	0.96	0.05	17.71	0.000
North-East	fungi:bacteria ratio	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	-0.02	0.02	-0.73	0.468	-0.03	0.04	-0.73	0.466
North-East	fungi:bacteria ratio	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.02	-0.18	0.854	0.00	0.02	-0.18	0.854
North-East	fungi:bacteria ratio	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.09	0.53	0.600	0.08	0.16	0.53	0.599
North-East	fungi:bacteria ratio	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.17	0.14	1.14	0.252	0.18	0.15	1.16	0.246
North-East	fungi:bacteria ratio	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.04	0.08	0.49	0.623	0.01	0.14	0.04	0.972
North-East	fungi:bacteria ratio	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.16	0.14	1.14	0.253	0.14	0.14	1.03	0.305
North-East	fungi:bacteria ratio	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	fungi:bacteria ratio	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	fungi:bacteria ratio	Lignin_content	fungi_bac	~	Lignin_content	c	0.11	0.10	1.08	0.279	0.16	0.14	1.10	0.274
North-East	fungi:bacteria ratio	Lignin_content	fungi_bac	~	LUI_historic	e	0.02	0.09	0.24	0.814	0.04	0.16	0.24	0.814
North-East	fungi:bacteria ratio	Lignin_content	fungi_bac	~	LUI_change	f	0.14	0.15	0.97	0.330	0.15	0.16	0.98	0.326
North-East	fungi:bacteria ratio	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	fungi:bacteria ratio	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	fungi:bacteria ratio	Lignin_content	fungi_bac	~~	fungi_bac		0.02	0.01	4.95	0.000	0.95	0.06	15.84	0.000
North-East	fungi:bacteria ratio	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.03	0.94	0.349	0.05	0.05	0.95	0.345
North-East	fungi:bacteria ratio	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.03	0.03	0.78	0.437	0.03	0.03	0.78	0.434
North-East	fungi:bacteria ratio	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.09	0.53	0.600	0.08	0.16	0.53	0.599
North-East	fungi:bacteria ratio	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.17	0.14	1.14	0.252	0.18	0.15	1.16	0.246
North-East	fungi:bacteria ratio	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.04	0.08	0.49	0.623	0.01	0.14	0.04	0.972
North-East	fungi:bacteria ratio	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.16	0.14	1.14	0.253	0.14	0.14	1.03	0.305
North-East	fungi:bacteria ratio	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	fungi:bacteria ratio	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	fungi:bacteria ratio	pH	fungi_bac	~	pH_historic	c	-0.08	0.07	-1.05	0.295	-0.14	0.13	-1.06	0.291
North-East	fungi:bacteria ratio	pH	fungi_bac	~	pH_change	d	-0.35	0.19	-1.86	0.064	-0.25	0.13	-1.91	0.056
North-East	fungi:bacteria ratio	pH	fungi_bac	~	LUI_historic	e	0.02	0.09	0.18	0.859	0.03	0.15	0.18	0.859
North-East	fungi:bacteria ratio	pH	fungi_bac	~	LUI_change	f	0.12	0.15	0.82	0.415	0.12	0.15	0.82	0.412
North-East	fungi:bacteria ratio	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	fungi:bacteria ratio	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	fungi:bacteria ratio	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	fungi:bacteria ratio	pH	fungi_bac	~~	fungi_bac		0.03	0.01	5.00	0.000	0.91	0.08	11.74	0.000
North-East	fungi:bacteria ratio	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi:bacteria ratio	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.13	0.898	0.00	0.02	0.13	0.898
North-East	fungi:bacteria ratio	pH	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.04	-0.39	0.693	-0.01	0.04	-0.39	0.693
North-East	fungi:bacteria ratio	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.02	0.09	0.19	0.846	0.03	0.15	0.19	0.846
North-East	fungi:bacteria ratio	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.11	0.15	0.70	0.483	0.11	0.15	0.71	0.481
North-East	fungi:bacteria ratio	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.02	0.09	0.17	0.864	-0.02	0.14	-0.13	0.901
North-East	fungi:bacteria ratio	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.11	0.15	0.70	0.482	0.10	0.14	0.68	0.494

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
North-East	fungi	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	fungi	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	fungi	CWM_leaf_P	fungi	~	CWM_leafP_historic	c	-0.03	0.11	-0.25	0.804	-0.03	0.13	-0.25	0.804
North-East	fungi	CWM_leaf_P	fungi	~	CWM_leafP_change	d	-0.08	0.11	-0.72	0.471	-0.10	0.14	-0.72	0.469
North-East	fungi	CWM_leaf_P	fungi	~	LUI_historic	e	0.07	0.09	0.85	0.396	0.13	0.15	0.85	0.393
North-East	fungi	CWM_leaf_P	fungi	~	LUI_change	f	0.30	0.15	2.03	0.042	0.31	0.15	2.11	0.035
North-East	fungi	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	fungi	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	fungi	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	fungi	CWM_leaf_P	fungi	~~	fungi		0.03	0.01	5.00	0.000	0.90	0.08	11.12	0.000
North-East	fungi	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.00	-0.20	0.844	0.00	0.01	-0.20	0.844
North-East	fungi	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.67	0.504	0.02	0.04	0.67	0.502
North-East	fungi	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.09	0.84	0.401	0.13	0.15	0.84	0.398
North-East	fungi	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.33	0.15	2.23	0.025	0.33	0.14	2.34	0.019
North-East	fungi	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.07	0.09	0.77	0.441	-0.02	0.14	-0.13	0.894
North-East	fungi	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.33	0.15	2.24	0.025	0.28	0.13	2.15	0.032
North-East	fungi	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	fungi	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	fungi	CWM_MycInt	fungi	~	CWM_MycInt_historic	c	0.36	0.11	3.25	0.001	0.39	0.11	3.46	0.001
North-East	fungi	CWM_MycInt	fungi	~	CWM_MycInt_change	d	0.35	0.12	2.98	0.003	0.35	0.11	3.12	0.002
North-East	fungi	CWM_MycInt	fungi	~	LUI_historic	e	0.05	0.08	0.64	0.522	0.09	0.13	0.64	0.521
North-East	fungi	CWM_MycInt	fungi	~	LUI_change	f	0.30	0.14	2.14	0.032	0.28	0.13	2.19	0.029
North-East	fungi	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	fungi	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	fungi	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.94	0.000
North-East	fungi	CWM_MycInt	fungi	~~	fungi		0.02	0.00	5.00	0.000	0.68	0.10	6.58	0.000
North-East	fungi	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.06	0.04	1.52	0.129	0.09	0.06	1.54	0.123
North-East	fungi	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.05	0.06	-0.96	0.338	-0.05	0.05	-0.96	0.339
North-East	fungi	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.11	0.09	1.26	0.207	0.18	0.14	1.27	0.203
North-East	fungi	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.24	0.15	1.66	0.097	0.23	0.14	1.69	0.091
North-East	fungi	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.11	0.09	1.22	0.223	0.08	0.13	0.59	0.559
North-East	fungi	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.24	0.15	1.65	0.098	0.15	0.13	1.19	0.236
North-East	fungi	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	fungi	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	fungi	Plant_biomass	fungi	~	Plant_biomass	c	0.08	0.10	0.74	0.460	0.10	0.14	0.74	0.458
North-East	fungi	Plant_biomass	fungi	~	LUI_historic	e	0.06	0.09	0.66	0.510	0.10	0.15	0.66	0.509
North-East	fungi	Plant_biomass	fungi	~	LUI_change	f	0.32	0.15	2.19	0.028	0.33	0.14	2.29	0.022
North-East	fungi	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	fungi	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	fungi	Plant_biomass	fungi	~~	fungi		0.03	0.01	4.95	0.000	0.90	0.08	11.06	0.000
North-East	fungi	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.02	0.67	0.502	0.03	0.04	0.67	0.501
North-East	fungi	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.00	0.02	0.18	0.855	0.00	0.02	0.18	0.855
North-East	fungi	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.09	0.84	0.401	0.13	0.15	0.85	0.398
North-East	fungi	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.33	0.15	2.20	0.028	0.33	0.14	2.30	0.021
North-East	fungi	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.07	0.09	0.77	0.440	-0.02	0.14	-0.11	0.910
North-East	fungi	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.32	0.15	2.20	0.028	0.28	0.13	2.10	0.035
North-East	fungi	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	fungi	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	fungi	Lignin_content	fungi	~	Lignin_content	c	0.05	0.11	0.52	0.604	0.07	0.14	0.52	0.603
North-East	fungi	Lignin_content	fungi	~	LUI_historic	e	0.06	0.09	0.68	0.496	0.11	0.16	0.68	0.494
North-East	fungi	Lignin_content	fungi	~	LUI_change	f	0.31	0.15	2.10	0.036	0.32	0.15	2.19	0.029
North-East	fungi	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	fungi	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	fungi	Lignin_content	fungi	~~	fungi		0.03	0.01	4.95	0.000	0.91	0.08	11.35	0.000
North-East	fungi	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	fungi	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.01	0.02	0.50	0.617	0.02	0.04	0.50	0.617
North-East	fungi	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.03	0.47	0.638	0.01	0.03	0.47	0.637
North-East	fungi	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.09	0.84	0.401	0.13	0.15	0.85	0.398
North-East	fungi	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.33	0.15	2.20	0.028	0.33	0.14	2.30	0.021
North-East	fungi	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.07	0.09	0.77	0.440	-0.02	0.14	-0.11	0.910
North-East	fungi	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.32	0.15	2.20	0.028	0.28	0.13	2.10	0.035

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
North-East	fungi	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	fungi	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	fungi	pH	fungi	~	pH_historic	c	-0.08	0.07	-1.07	0.287	-0.14	0.13	-1.08	0.282
North-East	fungi	pH	fungi	~	pH_change	d	-0.01	0.19	-0.06	0.956	-0.01	0.14	-0.06	0.956
North-East	fungi	pH	fungi	~	LUI_historic	e	0.06	0.09	0.75	0.454	0.11	0.15	0.75	0.452
North-East	fungi	pH	fungi	~	LUI_change	f	0.30	0.15	2.04	0.042	0.30	0.14	2.12	0.034
North-East	fungi	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	fungi	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	fungi	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	fungi	pH	fungi	~~	fungi		0.03	0.01	5.00	0.000	0.90	0.08	11.51	0.000
North-East	fungi	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	fungi	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	0.13	0.898	0.00	0.02	0.13	0.898
North-East	fungi	pH	LUI_change_in	:=	b*d	LUI_change_in	0.00	0.01	-0.06	0.956	0.00	0.01	-0.06	0.956
North-East	fungi	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.09	0.76	0.447	0.11	0.15	0.76	0.445
North-East	fungi	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.30	0.15	2.04	0.042	0.30	0.14	2.12	0.034
North-East	fungi	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.06	0.09	0.70	0.485	-0.02	0.14	-0.12	0.907
North-East	fungi	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.29	0.14	2.04	0.042	0.25	0.13	1.94	0.053
North-East	ergosterol	CWM_leaf_P	CWM_leafP_historic	~	LUI_historic	a	0.03	0.11	0.32	0.747	0.05	0.14	0.32	0.747
North-East	ergosterol	CWM_leaf_P	CWM_leafP_change	~	LUI_change	b	-0.30	0.17	-1.77	0.077	-0.24	0.13	-1.82	0.068
North-East	ergosterol	CWM_leaf_P	Ergosterol	~	CWM_leafP_historic	c	-0.12	0.09	-1.33	0.183	-0.17	0.13	-1.35	0.178
North-East	ergosterol	CWM_leaf_P	Ergosterol	~	CWM_leafP_change	d	0.04	0.09	0.43	0.664	0.06	0.13	0.44	0.664
North-East	ergosterol	CWM_leaf_P	Ergosterol	~	LUI_historic	e	0.06	0.07	0.87	0.383	0.12	0.14	0.88	0.380
North-East	ergosterol	CWM_leaf_P	Ergosterol	~	LUI_change	f	0.36	0.13	2.91	0.004	0.43	0.14	3.13	0.002
North-East	ergosterol	CWM_leaf_P	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	ergosterol	CWM_leaf_P	CWM_leafP_historic	~~	CWM_leafP_historic		0.05	0.01	5.00	0.000	1.00	0.01	77.51	0.000
North-East	ergosterol	CWM_leaf_P	CWM_leafP_change	~~	CWM_leafP_change		0.04	0.01	5.00	0.000	0.94	0.07	14.57	0.000
North-East	ergosterol	CWM_leaf_P	Ergosterol	~~	Ergosterol		0.02	0.00	5.00	0.000	0.83	0.10	8.59	0.000
North-East	ergosterol	CWM_leaf_P	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	ergosterol	CWM_leaf_P	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	ergosterol	CWM_leaf_P	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.01	-0.31	0.754	-0.01	0.03	-0.31	0.753
North-East	ergosterol	CWM_leaf_P	LUI_change_in	:=	b*d	LUI_change_in	-0.01	0.03	-0.42	0.673	-0.01	0.03	-0.42	0.673
North-East	ergosterol	CWM_leaf_P	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.07	0.81	0.419	0.12	0.14	0.81	0.417
North-East	ergosterol	CWM_leaf_P	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.35	0.12	2.88	0.004	0.41	0.13	3.09	0.002
North-East	ergosterol	CWM_leaf_P	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.07	0.72	0.474	-0.06	0.14	-0.43	0.667
North-East	ergosterol	CWM_leaf_P	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.35	0.12	2.89	0.004	0.36	0.12	2.97	0.003
North-East	ergosterol	CWM_MycInt	CWM_MycInt_historic	~	LUI_historic	a	0.16	0.09	1.72	0.086	0.24	0.13	1.77	0.077
North-East	ergosterol	CWM_MycInt	CWM_MycInt_change	~	LUI_change	b	-0.15	0.15	-1.01	0.311	-0.14	0.14	-1.02	0.306
North-East	ergosterol	CWM_MycInt	Ergosterol	~	CWM_MycInt_historic	c	0.11	0.10	1.04	0.301	0.14	0.13	1.04	0.297
North-East	ergosterol	CWM_MycInt	Ergosterol	~	CWM_MycInt_change	d	0.13	0.11	1.19	0.236	0.16	0.13	1.20	0.231
North-East	ergosterol	CWM_MycInt	Ergosterol	~	LUI_historic	e	0.05	0.08	0.65	0.514	0.10	0.15	0.66	0.513
North-East	ergosterol	CWM_MycInt	Ergosterol	~	LUI_change	f	0.32	0.13	2.55	0.011	0.37	0.14	2.70	0.007
North-East	ergosterol	CWM_MycInt	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	ergosterol	CWM_MycInt	CWM_MycInt_historic	~~	CWM_MycInt_historic		0.04	0.01	5.00	0.000	0.94	0.06	14.99	0.000
North-East	ergosterol	CWM_MycInt	CWM_MycInt_change	~~	CWM_MycInt_change		0.03	0.01	5.00	0.000	0.98	0.04	24.93	0.000
North-East	ergosterol	CWM_MycInt	Ergosterol	~~	Ergosterol		0.02	0.00	5.00	0.000	0.86	0.09	9.43	0.000
North-East	ergosterol	CWM_MycInt	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	ergosterol	CWM_MycInt	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	ergosterol	CWM_MycInt	LUI_hist_in	:=	a*c	LUI_hist_in	0.02	0.02	0.89	0.376	0.03	0.04	0.89	0.373
North-East	ergosterol	CWM_MycInt	LUI_change_in	:=	b*d	LUI_change_in	-0.02	0.03	-0.77	0.441	-0.02	0.03	-0.77	0.441
North-East	ergosterol	CWM_MycInt	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.07	0.07	0.89	0.375	0.13	0.15	0.89	0.372
North-East	ergosterol	CWM_MycInt	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.30	0.13	2.39	0.017	0.35	0.14	2.52	0.012
North-East	ergosterol	CWM_MycInt	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.06	0.07	0.81	0.416	-0.02	0.14	-0.15	0.879
North-East	ergosterol	CWM_MycInt	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.30	0.12	2.39	0.017	0.30	0.13	2.30	0.021
North-East	ergosterol	Plant_biomass	Plant_biomass	~	LUI_historic	a	0.19	0.12	1.61	0.109	0.25	0.15	1.65	0.100
North-East	ergosterol	Plant_biomass	Plant_biomass	~	LUI_change	b	0.04	0.20	0.19	0.850	0.03	0.15	0.19	0.850
North-East	ergosterol	Plant_biomass	Ergosterol	~	Plant_biomass	c	0.22	0.08	2.67	0.008	0.34	0.12	2.81	0.005
North-East	ergosterol	Plant_biomass	Ergosterol	~	LUI_historic	e	0.01	0.07	0.10	0.919	0.02	0.14	0.10	0.919
North-East	ergosterol	Plant_biomass	Ergosterol	~	LUI_change	f	0.31	0.12	2.65	0.008	0.37	0.13	2.79	0.005
North-East	ergosterol	Plant_biomass	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	ergosterol	Plant_biomass	Plant_biomass	~~	Plant_biomass		0.05	0.01	4.95	0.000	0.94	0.06	14.84	0.000
North-East	ergosterol	Plant_biomass	Ergosterol	~~	Ergosterol		0.02	0.00	4.95	0.000	0.77	0.11	7.26	0.000
North-East	ergosterol	Plant_biomass	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	ergosterol	Plant_biomass	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	ergosterol	Plant_biomass	LUI_hist_in	:=	a*c	LUI_hist_in	0.04	0.03	1.38	0.169	0.09	0.06	1.40	0.162
North-East	ergosterol	Plant_biomass	LUI_change_in	:=	b*c	LUI_change_in	0.01	0.05	0.19	0.851	0.01	0.05	0.19	0.850
North-East	ergosterol	Plant_biomass	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.07	0.67	0.503	0.10	0.15	0.67	0.501
North-East	ergosterol	Plant_biomass	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.32	0.13	2.55	0.011	0.38	0.14	2.71	0.007
North-East	ergosterol	Plant_biomass	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.04	0.07	0.59	0.557	-0.06	0.14	-0.45	0.656
North-East	ergosterol	Plant_biomass	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.32	0.13	2.55	0.011	0.34	0.13	2.65	0.008

Table S6.2 continued

Region	MO variable	mediator	lhs	op	rhs	label	est	se	z	*P*	est.std	se.std	z.std	*P* .std
North-East	ergosterol	Lignin_content	Lignin_content	~	LUI_historic	a	0.22	0.12	1.87	0.062	0.29	0.15	1.93	0.054
North-East	ergosterol	Lignin_content	Lignin_content	~	LUI_change	b	0.22	0.20	1.11	0.265	0.17	0.15	1.13	0.260
North-East	ergosterol	Lignin_content	Ergosterol	~	Lignin_content	c	0.12	0.09	1.34	0.181	0.18	0.13	1.36	0.175
North-East	ergosterol	Lignin_content	Ergosterol	~	LUI_historic	e	0.02	0.08	0.32	0.753	0.05	0.15	0.32	0.752
North-East	ergosterol	Lignin_content	Ergosterol	~	LUI_change	f	0.30	0.13	2.35	0.019	0.35	0.14	2.47	0.014
North-East	ergosterol	Lignin_content	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.77	0.006	-0.43	0.12	-3.70	0.000
North-East	ergosterol	Lignin_content	Lignin_content	~~	Lignin_content		0.05	0.01	4.95	0.000	0.93	0.07	13.39	0.000
North-East	ergosterol	Lignin_content	Ergosterol	~~	Ergosterol		0.02	0.00	4.95	0.000	0.85	0.09	8.99	0.000
North-East	ergosterol	Lignin_content	LUI_historic	~~	LUI_historic		0.08	0.02	4.95	0.000	1.00	0.00	NA	NA
North-East	ergosterol	Lignin_content	LUI_change	~~	LUI_change		0.03	0.01	4.95	0.000	1.00	0.00	NA	NA
North-East	ergosterol	Lignin_content	LUI_hist_in	:=	a*c	LUI_hist_in	0.03	0.02	1.09	0.277	0.05	0.05	1.10	0.273
North-East	ergosterol	Lignin_content	LUI_change_in	:=	b*c	LUI_change_in	0.03	0.03	0.86	0.392	0.03	0.04	0.87	0.386
North-East	ergosterol	Lignin_content	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.05	0.07	0.67	0.503	0.10	0.15	0.67	0.501
North-East	ergosterol	Lignin_content	LUI_change_te	:=	f+(b*c)	LUI_change_te	0.32	0.13	2.55	0.011	0.38	0.14	2.71	0.007
North-East	ergosterol	Lignin_content	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*c)	LUI_hist_tc	0.04	0.07	0.59	0.557	-0.06	0.14	-0.45	0.656
North-East	ergosterol	Lignin_content	LUI_change_tc	:=	f+(b*c)+(g*e)+(g*a*c)	LUI_change_tc	0.32	0.13	2.55	0.011	0.34	0.13	2.65	0.008
North-East	ergosterol	pH	pH_historic	~	LUI_historic	a	-0.02	0.16	-0.13	0.897	-0.02	0.14	-0.13	0.897
North-East	ergosterol	pH	pH_change	~	LUI_change	b	0.04	0.10	0.40	0.686	0.06	0.14	0.40	0.686
North-East	ergosterol	pH	Ergosterol	~	pH_historic	c	-0.12	0.05	-2.26	0.024	-0.27	0.12	-2.32	0.020
North-East	ergosterol	pH	Ergosterol	~	pH_change	d	0.38	0.14	2.72	0.007	0.33	0.12	2.84	0.005
North-East	ergosterol	pH	Ergosterol	~	LUI_historic	e	0.06	0.06	0.89	0.375	0.12	0.13	0.89	0.373
North-East	ergosterol	pH	Ergosterol	~	LUI_change	f	0.28	0.11	2.56	0.010	0.34	0.13	2.66	0.008
North-East	ergosterol	pH	LUI_historic	~~	LUI_change	g	-0.02	0.01	-2.80	0.005	-0.43	0.12	-3.74	0.000
North-East	ergosterol	pH	pH_historic	~~	pH_historic		0.10	0.02	5.00	0.000	1.00	0.01	193.05	0.000
North-East	ergosterol	pH	pH_change	~~	pH_change		0.01	0.00	5.00	0.000	1.00	0.02	62.03	0.000
North-East	ergosterol	pH	Ergosterol	~~	Ergosterol		0.01	0.00	5.00	0.000	0.72	0.11	6.83	0.000
North-East	ergosterol	pH	LUI_historic	~~	LUI_historic		0.08	0.02	5.00	0.000	1.00	0.00	NA	NA
North-East	ergosterol	pH	LUI_change	~~	LUI_change		0.03	0.01	5.00	0.000	1.00	0.00	NA	NA
North-East	ergosterol	pH	LUI_hist_in	:=	a*c	LUI_hist_in	0.00	0.02	0.13	0.897	0.01	0.04	0.13	0.897
North-East	ergosterol	pH	LUI_change_in	:=	b*d	LUI_change_in	0.02	0.04	0.40	0.690	0.02	0.05	0.40	0.688
North-East	ergosterol	pH	LUI_hist_te	:=	e+(a*c)	LUI_hist_te	0.06	0.07	0.89	0.374	0.12	0.14	0.89	0.373
North-East	ergosterol	pH	LUI_change_te	:=	f+(b*d)	LUI_change_te	0.29	0.11	2.56	0.011	0.36	0.13	2.68	0.007
North-East	ergosterol	pH	LUI_hist_tc	:=	e+(a*c)+(g*f)+(g*b*d)	LUI_hist_tc	0.05	0.07	0.81	0.420	-0.03	0.14	-0.24	0.814
North-East	ergosterol	pH	LUI_change_tc	:=	f+(b*d)+(g*e)+(g*a*c)	LUI_change_tc	0.29	0.11	2.56	0.011	0.31	0.12	2.46	0.014

Table S6.3: R^2 values of SEMs in Schwäbische Alb (South-West), Hainich-Dün (Central) and Schorfheide-Chorin (North-East). Given are the R^2 values for endogenous variables, i.e. the historic (mediator$_h$) and the change (mediator$_\Delta$) of a mediator variable and the soil microbial response variable (MO variable).

Region	MO variable	mediator	R^2 mediator$_h$	R^2 mediator$_\Delta$	R^2 MO variable
South-West	Cmic	CWM leaf P	0.52	0.01	0.12
South-West	Cmic	CWM MycInt	0.08	0.09	0.15
South-West	Cmic	Plant biomass	NA	0.03	0.21
South-West	Cmic	Lignin content	NA	0.01	0.07
South-West	Cmic	pH	0.01	0.00	0.14
South-West	Cmic	CWM leaf P	0.52	0.01	0.12
South-West	Cmic	CWM MycInt	0.08	0.09	0.15
South-West	Cmic	Plant biomass	NA	0.03	0.21
South-West	Cmic	Lignin content	NA	0.01	0.07
South-West	Cmic	pH	0.01	0.00	0.14
South-West	Nmic	CWM leaf P	0.52	0.01	0.14
South-West	Nmic	CWM MycInt	0.08	0.09	0.17
South-West	Nmic	Plant biomass	NA	0.03	0.21
South-West	Nmic	Lignin content	NA	0.01	0.08
South-West	Nmic	pH	0.01	0.00	0.17
South-West	Cmic:Nmic ratio	CWM leaf P	0.52	0.01	0.06
South-West	Cmic:Nmic ratio	CWM MycInt	0.08	0.09	0.08
South-West	Cmic:Nmic ratio	Plant biomass	NA	0.03	0.09
South-West	Cmic:Nmic ratio	Lignin content	NA	0.01	0.04
South-West	Cmic:Nmic ratio	pH	0.01	0.00	0.12
South-West	Pmic	CWM leaf P	0.55	0.03	0.24
South-West	Pmic	CWM MycInt	0.06	0.07	0.25
South-West	Pmic	Plant biomass	NA	0.07	0.26
South-West	Pmic	Lignin content	NA	0.04	0.21
South-West	Pmic	pH	0.04	0.01	0.25
South-West	beta-glucosidase	CWM leaf P	0.52	0.01	0.12
South-West	beta-glucosidase	CWM MycInt	0.08	0.09	0.13
South-West	beta-glucosidase	Plant biomass	NA	0.03	0.17
South-West	beta-glucosidase	Lignin content	NA	0.01	0.12
South-West	beta-glucosidase	pH	0.01	0.00	0.27
South-West	beta-xylosidase	CWM leaf P	0.52	0.01	0.28
South-West	beta-xylosidase	CWM MycInt	0.08	0.09	0.12
South-West	beta-xylosidase	Plant biomass	NA	0.03	0.12
South-West	beta-xylosidase	Lignin content	NA	0.01	0.11
South-West	beta-xylosidase	pH	0.01	0.00	0.32
South-West	chitinase	CWM leaf P	0.52	0.01	0.28
South-West	chitinase	CWM MycInt	0.08	0.09	0.12
South-West	chitinase	Plant biomass	NA	0.03	0.12
South-West	chitinase	Lignin content	NA	0.01	0.11
South-West	chitinase	pH	0.01	0.00	0.32
South-West	urease	CWM leaf P	0.52	0.01	0.18
South-West	urease	CWM MycInt	0.08	0.09	0.17
South-West	urease	Plant biomass	NA	0.03	0.04
South-West	urease	Lignin content	NA	0.01	0.05
South-West	urease	pH	0.01	0.00	0.04
South-West	DEA	CWM leaf P	0.52	0.01	0.35
South-West	DEA	CWM MycInt	0.08	0.09	0.24
South-West	DEA	Plant biomass	NA	0.03	0.22
South-West	DEA	Lignin content	NA	0.01	0.22
South-West	DEA	pH	0.01	0.00	0.29

Table S6.3 continued

Region	MO variable	mediator	R^2 mediator$_h$	R^2 mediator$_\Delta$	R^2 MO variable
South-West	phosphatase	CWM leaf P	0.52	0.01	0.06
South-West	phosphatase	CWM MycInt	0.08	0.09	0.08
South-West	phosphatase	Plant biomass	NA	0.03	0.03
South-West	phosphatase	Lignin content	NA	0.01	0.14
South-West	phosphatase	pH	0.01	0.00	0.63
South-West	bacteria	CWM leaf P	0.52	0.01	0.06
South-West	bacteria	CWM MycInt	0.08	0.09	0.08
South-West	bacteria	Plant biomass	NA	0.03	0.03
South-West	bacteria	Lignin content	NA	0.01	0.04
South-West	bacteria	pH	0.01	0.00	0.16
South-West	fungi:bacteria ratio	CWM leaf P	0.52	0.01	0.23
South-West	fungi:bacteria ratio	CWM MycInt	0.08	0.09	0.14
South-West	fungi:bacteria ratio	Plant biomass	NA	0.03	0.11
South-West	fungi:bacteria ratio	Lignin content	NA	0.01	0.11
South-West	fungi:bacteria ratio	pH	0.01	0.00	0.19
South-West	fungi	CWM leaf P	0.52	0.01	0.12
South-West	fungi	CWM MycInt	0.08	0.09	0.14
South-West	fungi	Plant biomass	NA	0.03	0.08
South-West	fungi	Lignin content	NA	0.01	0.09
South-West	fungi	pH	0.01	0.00	0.07
South-West	ergosterol	CWM leaf P	0.52	0.01	0.26
South-West	ergosterol	CWM MycInt	0.08	0.09	0.26
South-West	ergosterol	Plant biomass	NA	0.03	0.18
South-West	ergosterol	Lignin content	NA	0.01	0.22
South-West	ergosterol	pH	0.01	0.00	0.17
Central	Cmic	CWM leaf P	0.41	0.00	0.09
Central	Cmic	CWM MycInt	0.02	0.00	0.13
Central	Cmic	Plant biomass	NA	0.02	0.10
Central	Cmic	Lignin content	NA	0.01	0.08
Central	Cmic	pH	0.00	0.02	0.11
Central	Nmic	CWM leaf P	0.41	0.00	0.22
Central	Nmic	CWM MycInt	0.02	0.00	0.22
Central	Nmic	Plant biomass	NA	0.02	0.21
Central	Nmic	Lignin content	NA	0.01	0.22
Central	Nmic	pH	0.00	0.02	0.21
Central	Cmic:Nmic ratio	CWM leaf P	0.41	0.00	0.11
Central	Cmic:Nmic ratio	CWM MycInt	0.02	0.00	0.10
Central	Cmic:Nmic ratio	Plant biomass	NA	0.02	0.13
Central	Cmic:Nmic ratio	Lignin content	NA	0.01	0.11
Central	Cmic:Nmic ratio	pH	0.00	0.02	0.34

Table S6.3 continued

Region	**MO variable**	**mediator**	**R^2 mediator$_h$**	**R^2 mediator$_\Delta$**	**R^2 MO variable**
Central	Pmic	CWM leaf P	0.43	0.01	0.10
Central	Pmic	CWM MycInt	0.02	0.00	0.02
Central	Pmic	Plant biomass	NA	0.02	0.04
Central	Pmic	Lignin content	NA	0.02	0.01
Central	Pmic	pH	0.00	0.02	0.08
Central	beta-glucosidase	CWM leaf P	0.41	0.00	0.40
Central	beta-glucosidase	CWM MycInt	0.02	0.00	0.15
Central	beta-glucosidase	Plant biomass	NA	0.02	0.16
Central	beta-glucosidase	Lignin content	NA	0.01	0.11
Central	beta-glucosidase	pH	0.00	0.02	0.10
Central	beta-xylosidase	CWM leaf P	0.35	0.00	0.24
Central	beta-xylosidase	CWM MycInt	0.01	0.00	0.14
Central	beta-xylosidase	Plant biomass	NA	0.01	0.19
Central	beta-xylosidase	Lignin content	NA	0.01	0.19
Central	beta-xylosidase	pH	0.00	0.02	0.18
Central	chitinase	CWM leaf P	0.41	0.00	0.27
Central	chitinase	CWM MycInt	0.02	0.00	0.13
Central	chitinase	Plant biomass	NA	0.02	0.16
Central	chitinase	Lignin content	NA	0.01	0.20
Central	chitinase	pH	0.00	0.02	0.14
Central	urease	CWM leaf P	0.42	0.00	0.26
Central	urease	CWM MycInt	0.02	0.01	0.16
Central	urease	Plant biomass	NA	0.00	0.11
Central	urease	Lignin content	NA	0.02	0.25
Central	urease	pH	0.01	0.02	0.12
Central	DEA	CWM leaf P	0.41	0.00	0.10
Central	DEA	CWM MycInt	0.02	0.00	0.08
Central	DEA	Plant biomass	NA	0.02	0.29
Central	DEA	Lignin content	NA	0.01	0.09
Central	DEA	pH	0.00	0.02	0.10
Central	phosphatase	CWM leaf P	0.41	0.00	0.16
Central	phosphatase	CWM MycInt	0.02	0.00	0.11
Central	phosphatase	Plant biomass	NA	0.02	0.15
Central	phosphatase	Lignin content	NA	0.01	0.13
Central	phosphatase	pH	0.00	0.02	0.15
Central	bacteria	CWM leaf P	0.41	0.00	0.05
Central	bacteria	CWM MycInt	0.02	0.00	0.23
Central	bacteria	Plant biomass	NA	0.02	0.21
Central	bacteria	Lignin content	NA	0.01	0.06
Central	bacteria	pH	0.00	0.02	0.11
Central	fungi:bacteria ratio	CWM leaf P	0.41	0.00	0.29
Central	fungi:bacteria ratio	CWM MycInt	0.02	0.00	0.31
Central	fungi:bacteria ratio	Plant biomass	NA	0.02	0.31
Central	fungi:bacteria ratio	Lignin content	NA	0.01	0.31
Central	fungi:bacteria ratio	pH	0.00	0.02	0.31

Table S6.3 continued

Region	MO variable	mediator	R^2 mediator$_h$	R^2 mediator$_\Delta$	R^2 MO variable
Central	fungi	CWM leaf P	0.41	0.00	0.14
Central	fungi	CWM MycInt	0.02	0.00	0.22
Central	fungi	Plant biomass	NA	0.02	0.19
Central	fungi	Lignin content	NA	0.01	0.15
Central	fungi	pH	0.00	0.02	0.22
Central	ergosterol	CWM leaf P	0.41	0.01	0.08
Central	ergosterol	CWM MycInt	0.02	0.00	0.16
Central	ergosterol	Plant biomass	NA	0.02	0.07
Central	ergosterol	Lignin content	NA	0.02	0.14
Central	ergosterol	pH	0.00	0.04	0.13
North-East	Nmic	CWM leaf P	0.00	0.06	0.02
North-East	Nmic	CWM MycInt	0.06	0.02	0.03
North-East	Nmic	Plant biomass	NA	0.06	0.13
North-East	Nmic	Lignin content	NA	0.07	0.01
North-East	Nmic	pH	0.00	0.00	0.08
North-East	Cmic:Nmic ratio	CWM leaf P	0.00	0.06	0.13
North-East	Cmic:Nmic ratio	CWM MycInt	0.06	0.02	0.11
North-East	Cmic:Nmic ratio	Plant biomass	NA	0.06	0.15
North-East	Cmic:Nmic ratio	Lignin content	NA	0.07	0.09
North-East	Cmic:Nmic ratio	pH	0.00	0.00	0.34
North-East	Pmic	CWM leaf P	0.00	0.08	0.15
North-East	Pmic	CWM MycInt	0.10	0.01	0.32
North-East	Pmic	Plant biomass	NA	0.04	0.07
North-East	Pmic	Lignin content	NA	0.09	0.11
North-East	Pmic	pH	0.00	0.00	0.17
North-East	beta-glucosidase	CWM leaf P	0.00	0.06	0.05
North-East	beta-glucosidase	CWM MycInt	0.06	0.02	0.08
North-East	beta-glucosidase	Plant biomass	NA	0.06	0.05
North-East	beta-glucosidase	Lignin content	NA	0.07	0.05
North-East	beta-glucosidase	pH	0.00	0.00	0.28
North-East	beta-xylosidase	CWM leaf P	0.00	0.06	0.06
North-East	beta-xylosidase	CWM MycInt	0.06	0.02	0.15
North-East	beta-xylosidase	Plant biomass	NA	0.06	0.06
North-East	beta-xylosidase	Lignin content	NA	0.07	0.06
North-East	beta-xylosidase	pH	0.00	0.00	0.22
North-East	chitinase	CWM leaf P	0.00	0.06	0.17
North-East	chitinase	CWM MycInt	0.06	0.02	0.08
North-East	chitinase	Plant biomass	NA	0.06	0.08
North-East	chitinase	Lignin content	NA	0.07	0.08
North-East	chitinase	pH	0.00	0.00	0.18
North-East	urease	CWM leaf P	0.00	0.06	0.04
North-East	urease	CWM MycInt	0.06	0.02	0.07
North-East	urease	Plant Biomass	NA	0.06	0.02
North-East	urease	Lignin content	NA	0.07	0.02
North-East	urease	pH	0.00	0.00	0.50

Table S6.3 continued

Region	MO variable	mediator	R^2 mediator$_h$	R^2 mediator$_\Delta$	R^2 MO variable
North-East	DEA	CWM leaf P	0.00	0.06	0.15
North-East	DEA	CWM MycInt	0.06	0.02	0.31
North-East	DEA	Plant biomass	NA	0.06	0.01
North-East	DEA	Lignin content	NA	0.07	0.01
North-East	DEA	pH	0.00	0.00	0.52
North-East	phosphatase	CWM leaf P	0.00	0.06	0.25
North-East	phosphatase	CWM MycInt	0.06	0.02	0.19
North-East	phosphatase	Plant biomass	NA	0.06	0.13
North-East	phosphatase	Lignin content	NA	0.07	0.13
North-East	phosphatase	pH	0.00	0.00	0.25
North-East	bacteria	CWM leaf P	0.00	0.06	0.13
North-East	bacteria	CWM MycInt	0.06	0.02	0.31
North-East	bacteria	Plant biomass	NA	0.06	0.11
North-East	bacteria	Lignin content	NA	0.07	0.06
North-East	bacteria	pH	0.00	0.00	0.06
North-East	fungi:bacteria ratio	CWM leaf P	0.00	0.06	0.21
North-East	fungi:bacteria ratio	CWM MycInt	0.06	0.02	0.08
North-East	fungi:bacteria ratio	Plant biomass	NA	0.06	0.04
North-East	fungi:bacteria ratio	Lignin content	NA	0.07	0.05
North-East	fungi:bacteria ratio	pH	0.00	0.00	0.09
North-East	fungi	CWM leaf P	0.00	0.06	0.10
North-East	fungi	CWM MycInt	0.06	0.02	0.32
North-East	fungi	Plant biomass	NA	0.06	0.10
North-East	fungi	Lignin content	NA	0.07	0.10
North-East	fungi	pH	0.00	0.00	0.10
North-East	ergosterol	CWM leaf P	0.00	0.06	0.17
North-East	ergosterol	CWM MycInt	0.06	0.02	0.14
North-East	ergosterol	Plant biomass	NA	0.06	0.23
North-East	ergosterol	Lignin content	NA	0.07	0.15
North-East	ergosterol	pH	0.00	0.00	0.28