We thank the referee for his/her thorough review and valuable comments. We considered them one by one with great care and address them here with the hope for better clarity.
Referee comments are in blue.

1. Introduction:

Authors have started this section by introducing the causes of fresh ecosystem degradation as result of nutrient input along with detrital riverine/ aeolian input. However, they ended up with the determination of organic matter sources and extent of degradation in a soil horizon. The connectivity between organic matter source and concerned with freshwater ecosystems has not been addressed. This aspect needs to be elaborated in the discussion or modify the introductory part for better coherence.

Our aim of the study was to understand the implications of early degradation of organic material on isotopic tracer signatures in soils. These results we would then use to infer on interpretation of the sediment source attribution method. Hence the introduction is written in two parts; first, discussing the importance of sediment source attribution and the common tracers used in the technique. The other part addresses the issues of tracer stability during early degradation in soils, specifically the stability of long-chain fatty acid and *n*-alkanes after production and detachment, in terms of their carbon isotopic signature.

However, the reviewer raises a valid point and will considerably improve the coherence of the text, with less emphasis on the sediment source attribution and more focus on the stability of isotopic tracer signature. To address the connectivity between the stability of organic matter source signature and sediment tracing using CSIA in a freshwater ecosystem, we will include connecting sentences in the introduction section emphasizing the importance of understanding the stability of organic matter isotope signature in connection to CSIA based fingerprinting method.

2. Methodology:

A. Why inorganic carbon was not removed from the soil prior to bulk carbon isotope ratio measurement?

As the soils from forests with well-developed organic horizons are generally acidic, we expected no presence of inorganic carbon. To confirm that, we measured the pH of soils from all sites which was in the range of 3-4.2 (Page 3, line 16). Hence, it was not necessary to remove inorganic carbon from soils.

B. What is the recovery % of short and long-chain compounds in the entire extraction process?

We employed lipid extraction procedure utilizing high temperature (100°C) and high pressure (1500 psi) accelerated solvent extraction (ASE) technique. This technique has been adopted from many previous studies, which showed > 80% recovery of leaf and soil lipid biomarkers (Ardenghi et al., 2017; Jansen et al., 2006; Magill et al., 2015). We also employed 3 extraction cycles for every sample, each cycle with static hold of pressure and temperature (5 min) and solvent flushing, which has been suggested to be sufficient for > 80% recovery of lipids. In our study, we did not calculate the absolute recovery of lipids from samples, however approx. 70% of internal standard ($C_{19:0}$ FA) was recovered from the original amount added to the test samples before lipid extraction and compound separation.

C. How the methylation correction was applied for carbon isotope ratio measurement? Which formula was used and how the alcohol isotope ratio was measured?

Correction of measured FAMEs was done by mass balance for contribution of carbon added during methyl esterification to obtain the $\delta^{13}C$ value of fatty acid using following formula;

$$\delta^{13}C_{FA} = \frac{\delta^{13}C_{FAME} - (1-X)\delta^{13}C_{Methanol}}{X}$$

Where X is the ratio of carbon atoms in FA to the carbon atoms in corresponding FAME. $\delta^{13}C_{Methanol}$ was measured with an elemental analyser coupled to an isotope ratio mass spectrometer, using similar instrumental parameters as bulk C isotope analysis in our study. We added this information in the methods section to the final version of the manuscript.

3. Result:

A. The best way to show the result is against the respective soil profiles. The different zone identified in the different soil profiles can also be marked for clarity.

We do not clearly understand to which specific results the first point made by reviewer. However, if the reviewer suggest that the figure 5 (compound-specific isotope values) to be oriented vertically against soil horizons, we agree to the suggestion and modify it accordingly such that the trend of each compounds isotope values in the horizons placed next to each other from left to right. We will also define the organic horizons (Oi-Oe-Oa) in the method section for better clarity of the nomenclature of the horizons. Regarding the second comment, assuming it is also for figure 5, we will mark the horizon after which the isotopic signal remained stable.

B. What is LB pruce*?

$LB_{spruce*}$ is site no. 3 (Lake Baldegg catchment, Table 1) with spruce and moss as primary aboveground biomass sources and with organic horizon categorized as a raw humus. We will explain the site abbreviations in the caption of every relevant figure for better understanding.

C. At many places, you are writing d13C enrichment or depletion!! Please write an 'increase in δ13C or 'enrichment of 13C'.

Thank you for the correction, we will change the wording.

D. Why moss values are neglected? Why the significantly low δ13C values?

Mosses generally have lower $\delta^{13}C$ values than higher plants as they grow in wet and humid conditions and experience less water loss due to evapotranspiration. We did not neglect mosses as we did analyze their isotopic signatures. However, regarding the overall contribution to the humus layer material, we considered spruce to be a dominant source of biomass/lipids to the soils compared to moss at site $LB_{spruce*}$. Thus, for the calculation of magnitude of change in $\delta^{13}C$ value from fresh plant biomass to the mineral soil (Δ_1), only needle isotope value was considered to obtain the $\delta^{13}C_{\text{(fresh plant biomass)}}$ at site $LB_{spruce*}$. This was done to avoid overestimation of change/increase in $\delta^{13}C$, as moss isotope value is considerably depleted than that of spruce needle. Also, isotopic composition of soils is controlled by the amount of biomass from each source on a larger timescale. However, we have to admit, that we have no data to prove the dominance of needle biomass over moss biomass. We will thus formulate our interpretation a bit more cautiously.

4. Discussion:

A. Why the bulk δ13C and is showing 13C enrichment? Compared to the nC28 and nC29 B. Is the true for other long-chain fatty acids and alkanes as well?

A+B. The majority of the bulk organic matter is considered to be less recalcitrant and more readily available to soil organisms than long-chain alkanes and fatty acids. During degradation/mineralisation, bacteria (or rather the respective enzymes) have generally a higher affinity towards the lighter isotope, which will be preferentially fed on. Hence, we observed generally a greater enrichment in ^{13}C of the remaining bulk organic matter across different degradation stages. A second aspect is, that previous studies have shown that lipid biomolecules are depleted in ^{13}C compared to bulk organic matter due to the kinetic isotope effects during various biochemical reactions in lipid biosynthesis (Chikaraishi et al., 2004; Collister et al., 1994). Hence, we already observe lower $\delta^{13}C$ values in long-chain fatty acids and *n*-alkanes compared to the bulk $\delta^{13}C$ values (Page 6, line 7-8) before degradation even starts with fractionation processes.

References

Ardenghi, N., Mulch, A., Pross, J. and Maria Niedermeyer, E.: Leaf wax n-alkane extraction: An optimised procedure, Org. Geochem., 113, 283–292, doi:10.1016/j.orggeochem.2017.08.012, 2017.

Chikaraishi, Y., Naraoka, H. and Poulson, S. R.: Carbon and hydrogen isotopic fractionation during lipid biosynthesis in a higher plant (Cryptomeria japonica), Phytochemistry, 65(3), 323–330, doi:10.1016/j.phytochem.2003.12.003, 2004.

Collister, J. W., Rieley, G., Stern, B., Eglinton, G. and Fry, B.: Compound-specific δ 13C analyses of leaf lipids from plants with differing carbon dioxide metabolisms, Org. Geochem., 21(6), 619–627, doi:10.1016/0146-6380(94)90008-6, 1994.

Jansen, B., Nierop, K. G. J., Kotte, M. C., de Voogt, P. and Verstraten, J. M.: The applicability of accelerated solvent extraction (ASE) to extract lipid biomarkers from soils, Appl. Geochem., 21(6), 1006–1015, doi:10.1016/j.apgeochem.2006.02.021, 2006.

Magill, C. R., Denis, E. H. and Freeman, K. H.: Rapid sequential separation of sedimentary lipid biomarkers via selective accelerated solvent extraction, Org. Geochem., 88, 29–34, doi:10.1016/j.orggeochem.2015.07.009, 2015.