We are grateful for the positive evaluation of our work and the constructive suggestions to improve the quality of our manuscript. In the following, we reply as comprehensively as possible to each of the comments:

The manuscript submitted by Rummel and coworkers for publication in Biogeoscienes describes the role of litter quality for N2O as well as CO2 emissions as well as bacterial community structure. The authors used litter material from maize roots and shoots which were grown under different fertilization levels, applied the materials in a pot experiment to soil which was obtained from an agricultural field and measured for a period of 22 days gas fluxes as well as chemical parameters. At the end of the incubation period also bacterial community structure was analysed. As expected depending on the C:N ratio of the litter material and the availability of easily degradable materials gas emissions and N pools in soil changed, which was also reflected by shifts in bacterial community structure. The study is nicely performed and the data presented of interest, although not totally new. The paper is nicely written and the figures are clear. Like always in such experiments, there is the issue of water content, which was fixed to 50% max WHK, however other water contents would for sure change the results (mainly fluctuation water levels like observed in the field) and also the use of other soil types may induce different response patter. I think here the discussion must be adapted accordingly to make sure that this is showcase but not a general response.

We agree that soil moisture is an important control of N_2O emissions and changes in water content would affect results. Certainly, fluctuations of water content would induce different response patterns. We will address this topic in a respective paragraph in the discussion:

In addition to soil mineral N concentration and plant litter, soil type and soil moisture may have influenced our results (e.g. Aulakh et al., 1991). Increasing soil moisture leads to increasing N_2O emissions, but relative contribution of nitrification and denitrification to N_2O formation may change with increasing soil moisture (Bateman and Baggs, 2005; Baral et al., 2016; Li et al., 2016). Therefore, future experiments with different soil moisture contents should include methods to differentiate between N_2O formation pathways.

Furthermore there are several issues that need to be considered during revision 1. The description of the sequencing data is very poor. Neither basic data on reads quality rarefraction subsampling etc is given

In addition to the information you find in the manuscript, we included raw reads, reads after filtering, subsample size, observed ASVs, and diversity indices in Table S4 in the Supplementary that was published alongside the manuscript. Rarefaction curves of the observed

amplicon sequence variants (ASVs) of the soil inhabiting bacterial communities are displayed in Supplementary Fig. S1.

nor analysis of core microbiomes (together with responders) were made. I guess this is somehow a missed change and the paper would much benefit from a better integration of the molecular data.

As suggested, we analyzed the core microbiomes and respective responders and will include the following paragraphs in the manuscript. Due to size limitations core microbiome tables and Venn diagrams will be included in the Supplementary.

2.5.2 Sequence processing

The core microbiomes and respective responders have been analyzed on genus level, grouped by either the applied litter treatment or N fertilizer levels using the R package *ampvis2* v2.4.7.

3.5 Bacterial community structure

The most abundant genera attributed to the core microbiomes were *Pseudomonas*, *Altererythrobacter*, *Gaiella*, *Nocardioides*, *Agromyces*, *Bacillus*, and *Lysobacter*. Overall, 80 genera were attributed to the core microbiome, when grouped by N levels, while 21 genera and 6 genera were identified as responders to N1 and N2, respectively. In detail, the responders to the applied N treatment were, among others, the genera *Chthonibacter*, *Luteimonas*, *Sphingobium*, *Novosphingobium*, *Adhaeribacter*, *Nitrospira*, *Gemmata* and *Devosia* for N1 and *Conexibacter* for N2 samples. When grouped by litter treatment, the core microbiome comprised 77 genera accounting for 73% of the relative abundance, while 9, 3 and 10 genera were identified as responders to the applied litter treatment Control, Root and Root+Shoot, respectively. *Nonomuraea*, *Fluviicola* and *Nitrospira* responded to the Root+Shoot treatment, while the genera *Lapillicoccus* and *Adhaeribacter* responded to the Root treatment. The genera *Litorilinea*, *Gemmata*, *Novosphingobium* and *Opitutus* were identified as responders to the Control treatment. For N levels and litter treatments respectively, 833 and 838 genera were attributed to non-core microbiomes, accounting for 20% and 19.5% of relative abundance.

4.3 Bacterial community structures as affected by maize litter and soil N level

The most abundant phyla in our soil samples, *Actinobacteria*, *Proteobacteria* and *Chloroflexi,* were also affiliated to the core microbiomes. […]

Actinobacteria, *Chloroflexi*, and *Firmicutes* were more abundant in N2 samples, whereas *Bacteroidetes*, and *Nitrospirae* were more abundant in N1 samples which may indicate that the latter are more competitive under conditions of very low mineral nitrogen availability in soil. This

was further validated as *Nitrospira* (*Nitrospirae*), known to oxidize nitrite (Koch et al., 2015), was identified as a responder for N1 and -RS. […]

Species belonging to the genus *Agromyces* (*Actinobacteria*), which was affiliated to the core microbiomes, are also known to reduce nitrate (Zgurskaya et al., 2008). In addition, species capable of denitrification under anaerobic, O_2-limited and aerobic conditions can be found in the genera *Bacillus* and *Micromonospora*, as well as *Pseudomonas* and *Rhodococcus* (Verbaendert et al., 2011) that were affiliated to the core microbiome but were more abundant in N2 samples. The genus *Opitutus* was identified as responder to -Cn and comprises the bacterium *Optitutus terrae* that was only found in anoxic habitats in soils (Chin et al., 2001). […]

Further the sequencing data needs to be submitted to a public database.

The information on sequence data availability can be found under “Data availability” in line 449: “The 16S rRNA gene sequences were deposited in the National Centre for Biotechnology Information (NCBI) Sequence Read Archive (SRA) under bioproject number PRJNA557843.”

Finally it is general accepted that all DNA extraction kits contain contaminating DNA. Thus a water extraction control would be essential to remove contaminating OTUs from the data.

As described in line 164ff, we did not use a commercial DNA extraction kit. Instead the DNA extraction protocol by Griffiths et al. (2000) was used. All solutions were sterilized by either autoclaving or sterile filtration. In addition, controls for contamination were carried out during the extractions and in subsequent PCRs.

2. I miss data on bacterial abundance microbial biomass C and N etc. This information is required and the one hand as soil microbes are an important storage device for N. On the other hand all molecular data is relative, thus to translate the data to absolute numbers biomass values are needed.

We agree that it is highly likely that microbial biomass varies depending on litter input. Strong differences in CO_2 emissions between treatments indicate differences in microbial activity which could be reasoned by variations in microbial biomass and taxonomy. Nonetheless, the here presented study shows how microbial community composition responds to different litter inputs and whether the relative differences in microbial community structure can be related to CO_2 and N_2O emissions. However, in the here presented work, changes of microbial biomass were not in the scope of the research objective and therefore this data was not collected.

3. I am quite confused that only three replicates were used for molecular analysis, despite 4 replicates were used for each treatment.

We used all four replicates of each treatment for molecular analysis. However, for one replicate of N2-Rt, DNA concentration was too low and the 16S rRNA gene PCR was not successful, thus only the remaining three replicates of this treatment were evaluated. In addition to figure and table captions, we will include this information in Material & Methods section 2.5.2.

Further I wonder why only shoots from N2 were used and not shoots from N1 treatment.

To be able to compare the litter treatments over soil conditions, we had to use the same litter types for both soil N levels. We will specify our choices in Materials & Methods section 2.2:

The incubation experiment consisted of a two-factorial setup comprising two N levels (N1 and N2) and three litter levels (Control = Cn, Root = Rt, Root+Shoot = RS) (see Table 1 and Figure 1 for details). To allow comparison of litter treatments over soil conditions, the same litter types for both soil N levels were used. As N2 plants had produced greater and healthier biomass during pre-experimental growth phase, only N2 shoots were used for both soils. Roots from N1 and N2 plants were mixed to ensure sufficient amounts for all replicates. […]

4. The provided hypothesis is very generic and I guess it must be specified as it is quite obvious that the degree of label materials influences process rates in soil.

We will specify our hypotheses as following: We hypothesize that differences in N_2O emissions between treatments can be related to degradability of maize litter with easier degradable shoot litter leading to higher N_2O formation. We further expect that differences in litter chemical quality are reflected in the structural composition of the soil microbial community with higher availability of N and C leading to a more specialized community.