Referee comment 2

We would like to thank Dr. Rudaya for her thoughtful comments and suggestions which will improve the clarity and the quality of the paper. Below, we addressed all comments and questions.

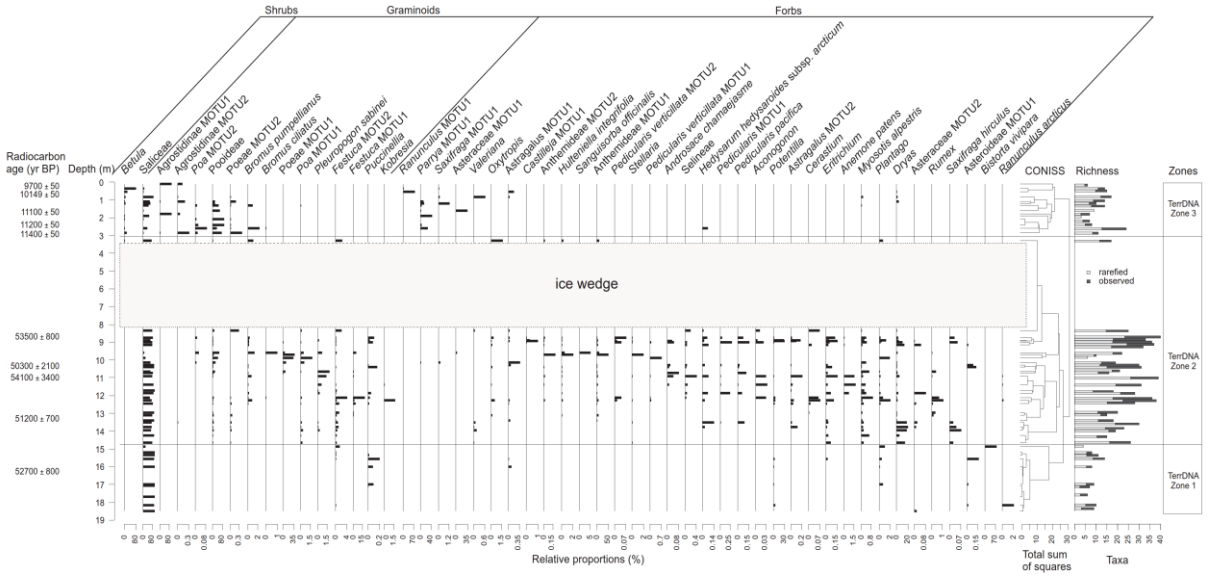
1. What was the source for the plant DNA? Is it possible to determine it? Is it chloroplast, nuclear or mitochondrial DNA? Pollen cells don't contain chloroplasts and if it was possible to determine chloroplast DNA it would be a very reliable method for separation of local and not-local plant taxa.

The targeted DNA sequence is the *trnL*-UAA P6-loop (Taberlet et al. 2007), which is located on the chloroplast genome of plants. As already answered in the discussion forum by Referee 3, chloroplast genomes are indeed present in pollen and therefore (unfortunately) cannot be used to separate local from non-local plant taxa. We decided to address this point briefly in the discussion of the manuscript.

2. I don't like how the sedaDNA and pollen diagrams ('stratigrams') are structured. It is very hard to find any taxa on them. I suggest structuring them in ecological way – herbs, shrubs, trees etc. or explain what the principle of such structure was.

We agree and will rearrange all stratigraphic diagrams in the suggested manner. However, within the groups we would like to retain the original sorting.

The diagrams were plotted using the R command *strat.plot* from the package rioja (Juggins, 2012) and sorted using wa.order. Our intention was to better visualize the changes in species composition from the top of the core to the bottom. We hope that this compromise between an ecological meaningful structure and the application of wa.order is acceptable. The following diagram shows an example of the new version:



3. I suspect that in the lower stratigraphical zones pollen and other material can be redeposited. Radiocarbon dating, amount of pre-Quaternary pollen and spores indirectly confirm this suggestion. How do you explain the inversion in radiocarbon dates? Maybe, it is contamination from the lower more ancient layers? Why do you not use pollen concentrations that can be an additional marker of redeposition?

Thank you for this suggestion and we agree. According to Schirrmeister et al. (2016) the deepest 2.5m of the core imply a former (ancient) active layer. An active layer is prone to disturbances such as erosion, cryoturbation (through seasonal thawing and re-freezing) and potentially also grazing, all of which allow for re-deposition of older material. In the deepest 2.5m the amount of pre-Quaternary pollen and spores is highest (up to ~5%) among all samples and give weight to your suggestion. For the rest of the core the amount of pre-Quaternary pollen and spores is lower. Furthermore, the radiocarbon dating is at its limit and therefore associated with high standard deviations. We will include the suggested pollen concentrations in the corresponding results section and will address this issue in the discussion. We will also include its implication on the sedaDNA record.

What part of the core contains higher percentages of exotic DNA sequences (contamination)?

Exotic DNA sequences were found in almost all samples, extraction blanks and PCR negative controls and are reported in S5_cultivated_nonArctic_plants.xlsx. The highest contribution of exotic DNA sequence counts were found at 2.85m depth. We realized that we forgot to change the original sample names with the corresponding depths in the supplementary tables. We apologize for this and will add this information.

4. What taxa belong to NPPs in this study? Page 9, line 21: 'pollen, spores and non-pollen palynomorphs (NPPs)'. Table 3 ('Number of non-pollen palynomorphs for each sample') contains algae, fungi, mosses, ferns (!), lycopods (!) and pre-Quaternary spores (!). Page 17, lines 13-14: 'A total of 1,092 NPPs were counted and assigned to 25 taxa, comprising four mosses, two spikemosses, six clubmosses, three ferns, six fungi and four green algae'. Usually, in pollen study to NPPs belong fungi, algae, remnants and eggs of animals etc.; objects which can be determined in the pollen slide after chemical treatment. Spores of higher vascular plants don't relate to NPPs (as a rule, but you can explain your position).

Thank you for pointing this out. Of course you are right, only algae apply to this term and we mixed it up with the spores. We decided to omit the term NPP and instead use "spores and algae".

5. I didn't understand for what you calculated terrestrial-aquatic and Poaceae-Cyperaceae ratios. You did not use it in discussion. I didn't also realize where is the interpretation of the PCA analysis in this study.

Thank you for pointing this out, we agree and will discuss this now thoroughly in the manuscript. In some palynological studies the ratio of Poaceae to Cyperaceae is used to assess temporal changes in humidity. We applied this ratio to trace the hydrological development along the core since our results suggested the local presence of a shallow water body in several depths. However, since some Poaceae (e.g. *Arctophila fulva*/*Dupontia fisheri*) are associated with wet conditions while the Cyperaceae *Kobresia* is an indicator for (cryo-)arid climate we chose to compare this ratio with the terrestrial-aquatic ratio. Additionally, the ratios were an instrument to visualize and compare the contribution of terrestrial and swamp/aquatic taxa between samples as well as between the two proxies. We hope that we were able to make our intent clearer and that our reasoning is satisfactory.

6. I suggest constructing the age-depth model for the upper part of the core. CONISS reveals two pollen zones in upper Pleistocene-Holocene part (Fig. 6: TerrPZ3). Maybe, it is the border between YD and Boreal.

Thank you for this suggestion. We will perform the age-depth model with Bacon and implement it in the manuscript.

7. Where is S3? Page 12, lines 7-8: 'The complete taxa-list is available in S3'.

This was unintended and is a mistake. The complete list is available in S4. This will be corrected in the text.

8. How do you explain the hiatus between last radiocarbon date (9700±50 14C yr BP) on the depth of 0.3 m and modern sample on the depth of 0.1 m?

The permafrost core was drilled at the top of a Yedoma hill (Schirrmeister et al., 2016). Wind and rain probably eroded the younger deposits. We will include this and rephrase the beginning of the discussion chapter 5.3 in the manuscript from:
"The upper part of the core from the ice-wedge up to approximately 0.25 m depth includes the late glacial transition to the early Holocene (approximately 11.4 to 9.7 kyr BP, (13.4–11.1 cal kyr BP)). As emphasized in Andreev et al. (2011) records of the late glacial transition are rare because of active thermoerosion. Hence, our results provide valuable information about the vegetation history in this region and organic matter composition."

To:
"The permafrost core was drilled at the top of a Yedoma hill (Schirrmeister et al. 2016). Wind and rain probably eroded most of the Holocene deposits resulting in a hiatus between the sample of the modern core top and the second sample at 0.25 m depth (11.1 cal kyr BP). The upper part of the core consists of sediments dated to the transition from the late glacial to the early Holocene (13.4–11.1 cal kyr BP). As emphasized in Andreev et al. (2011) records of the late glacial transition are rare because of active thermoerosion. Hence, our results provide valuable information about the vegetation history in this region and organic matter composition."

<u>Specific comments:</u>
Page 1, line 28: 'a shrub tundra spectrum' – spectra (plural). One sample - one spectrum, several samples – several spectra. Or you should use 'pollen complex'.
We rephrased the sentence from:
"Pollen also records a shrub tundra spectrum, mostly seen as changes in relative proportions of the most dominant taxa, while a decrease in taxonomic richness was less pronounced compared to sedaDNA."

To:
"Pollen also records a shrub tundra community, mostly seen as changes in relative proportions of the most dominant taxa, while a decrease in taxonomic richness was less pronounced compared to sedaDNA."

Saliceae, Pooideae etc. are the tribes. Please, specify what nomenclature system you used in this study.
Indeed, we did not state the basis for the taxonomic assignment sufficiently clear. The taxonomic assignment for sedaDNA is based on the NCBI taxonomy. The taxonomic assignment is performed using the OBItools command *ecotag* (Boyer et al., 2016) which uses a Last Common Ancestor approach based on the NCBI taxonomy database (Sayers et al., 2009).

To clarify which system we used, we will add the following sentence on page 9 line 7:
"The nomenclature for the taxonomic assignment follows the NCBI taxonomy (Sayers et al., 2009)."

I found the mistakes in Latin. 'Osmuda' – Osmunda (everywhere) Polypodiaceae is the family mainly of tropical ferns. Use Polypodiophyta or specify what nomenclature system you used in this study. 'Botrycoccus' – Botryococcus (in the text) 'Cichorideae' – Cichoriodeae (Fig.6)
Thank you for pointing these out. We will correct this to Botryococcus and Cichoriodeae. We followed Andreev et al. (2011), who uses Polypodiaceae. But we will change this to Polypodiophyta.

Page 13, Line25. 'assigned to 21 swamp or aquatic taxa' . In S4 only 20.
This was unintended. The list is now corrected: Poinae was transferred from terrestrial to the swamp/aquatic list.

Page 15, Line 11: 'to 53 taxa, including indeterminable and pre-Quaternary pollen.' Indeterminable and pre-Quaternary pollen are not taxa and cannot be included in the taxa list.
This is true. We wanted to say the 53 taxa, the pre-quaternary pollen and indeterminable pollen sum up to a total of 8881 terrestrial pollen grains. We addressed this by changing the sentence to:

"A total of 8,580 terrestrial pollen grains were counted and ascribed to 53 taxa, while 248 were indeterminable and 53 assigned as pre-Quaternary pollen."

Page 19, Line 1: 'the under-representation of Salix in comparison to other plant functional types'. Plant functional type is the unit of biome reconstruction. You should rephrase this sentence.
We agree and with regard to shortening the paper (referee 3) we will discard the sentence and rephrase the paragraph.

Line 20: 'Compared to the number of vascular plant taxa (58) and bryophytes (20) recorded by pollen analysis'. Where is the list with moss taxa, determined by pollen analysis?
The list is included in Table 3. With regard to comment number 4 we will rephrase the sentence:
"Compared to the number of vascular plant taxa (58) and bryophytes (4) recorded by pollen analysis, the sedaDNA approach recorded a higher number of both vascular plants (134) and a bryophytes (20)."

Page 23. Line 27: 'In drier periods'. You have reliable chronology for the upper part. When were drier or wetter periods?
We agree. We will include the corresponding ages in the text, after building the age-depth model.

Page 24, Line 10: 'Published pollen records for 11.7–10.6 kyr BP are dominated by Cyperaceae and Poaceae. Shrub pollen increased at approximately 9 kyr BP (Andreev et al., 2011), with up to 60 %

of Betula in the Khorogor Valley near Tiksi (Andreev et al., 2011; Grosse et al., 2007). These results match well with the pollen data presented here.' It is not true. In your study Betula pollen increased at least 2 kyr earlier (Figs 2,6).

The pollen diagram Khg-11 in Grosse et al. (2007) shows an increase in *Betula* sect. Nanae of ~35% and *Betula* sect. Albae of ~25% at 11.540 ± 60 ^{14}C yr BP. In our study the increase is recorded at ~11.400 ± 50 ^{14}C yr BP. Hence, it does match well, but it was not clearly stated why. We therefore rephrased the sentence:

"Shrub pollen increased in the Laptev Sea region approximately at 9 kyr BP (Andreev et al., 2011), while in the Khorogor Valley near Tiksi an increase of Betula pollen up to 60% was recorded already at 11.54 kyr BP (Grosse et al., 2007; Khg-11)."

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