Referee Report

Since most of my previous questions have been addressed in the previous report, in this opportunity I will share some comments according to some of the facts given in the paper.

1. The title is broad when speaking about the diversity and community structure of alkane degrading bacteria. In the work you spoke about diversity at the Phylum level and I strongly believe this should be addressed in the title as well. If the title wants to remain as is, please include some Genus, or species information in the figures/analysis. This takes me to my next comment…
2. The metagenome data that has been mentioned has great potential and should be exploited a bit more. A small analysis that would include assembly and binning of contigs would be required but would give some information on WHO the organisms are. Only with this information can the DIVERSITY and community structure of ALKANE degrading bacteria be concluded. The data you have shown (figure 8) does not show that it is actually these organisms that change. In other words, the WHOLE community and diversity is changing but no conclusions can be drawn about only alkane degrading bacteria since your gene has low variation.
3. The introduction does not include enough information about littefall and why it is important to study this environment. It is not clear why the study was performed with this specific environment, unless you read other studies.
4. In the conclusions would it be appropriate to suggest some alkane bacteria activity assays from the environmental samples (RNA)?
5. I believe you have a typo in page 6, line 28: MEGA program instead of MAGA?
6. Figure 2 can be in the supplementary data?