**Chrats meeting**

* Figure with a lot of details --> make it a bit more simple and redirect to GitHub
* Plant biomass: it means that 1.0 MeJA is inducing even more stress than the positive control
* qPCR data: Arabidopsis has higher gene induction of LOX2 and MYC2 --> point for showing that we didn’t measure at the right time and it could have issues with the reviewer
* NMDS1: All data separating the data into 4, --> interesting in supplementary to show the bias that based on the conditions there are no differences in depth. Roots more depth and less diversity, and soil has less depth and more diversity
* PERMANOVA: Effects of treatment are not very strong and not differences in pairwise comparisons between the whole community
* Neutral Model Fit: 4 neutral models for each data slice, endosphere is not included as 3 samples were lost 1 root for one of the species and 1 root for all of the treatments. --> Possible to downsample by taking a few samples randomly and have an equal number to compare.
* NMDS Above expected cluster together: How is the species abundance of these ASVs? --> Rare species about the distribution in one sample. If take these Above species and rank their abundance across the samples? If you have low abundance organisms is more prone to be affected by depth issues
* Does the direction here indicates ?
* Neutral heat trees: --> keep those as main figures, and leave out the treatments. Pedro’s hypothesis, diversity into these two taxons (at Family level) is going to be relevant to the response to herbivores. --> Is great, to make it even more clear you can also show a negative situation (?). Show a high abundance family that doesn’t change at all between treatments
* If there’s anything close to 1 means that **all** members of these particular taxon are always selected --> diversity in this family is important to the response to stress. Pseudomonadales are not relevant for the subset