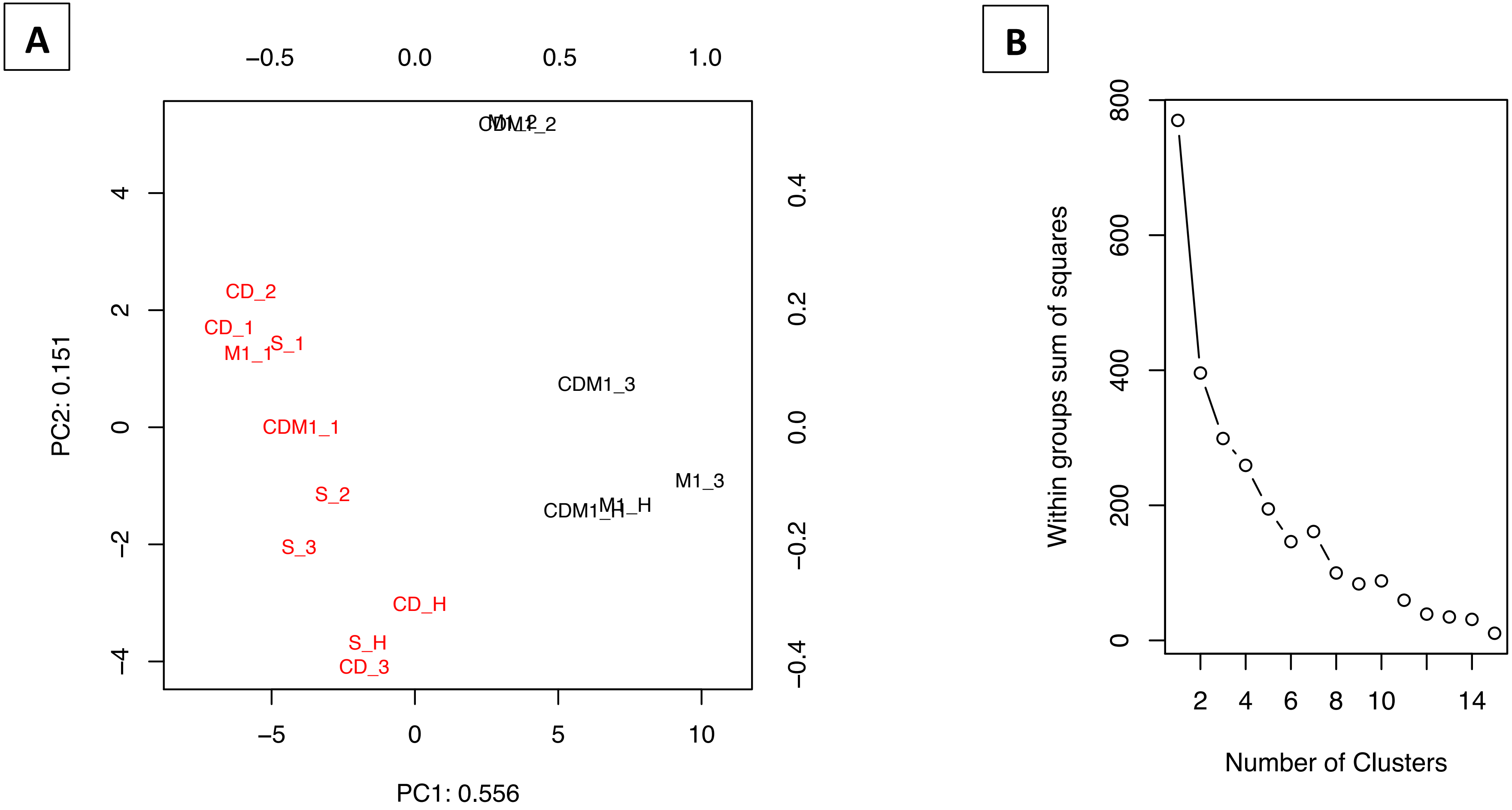

Fig. S2 - Compositional biplot and barplot of faecal samples. **(A)** PCA plot generated following a centered log-ratio transformation of the dataset. This plot simultaneously displays the distance relationships between samples (colored in black or red), and the variance of the taxa grouped at the genus level (AB). This is a form plot which maintains the relationships between samples. The sample names are colored by their Kmeans group membership using the default clustering method in R. **(B)** Sum of squares distances from the group centre, as a function of the number of clusters. The large difference between 1 cluster and 2 clusters, and the large proportion of variance explained on PC1 (>50%), supports the idea that this is a robust split. This major split is found to be between samples that have received MET-1 and those that have not. Note that samples receiving MET-1 at day 1 group with samples that did not receive MET1 because samples were collected from these mice before the MET-1 had time to transit the gut. The MET-1 and MET-1+C. diff gavaged mice at day two are in the top right corner of the plot, and are overlaid. This indicates that the composition of these samples are extremely similar. The day three, and harvest samples are also very similar.