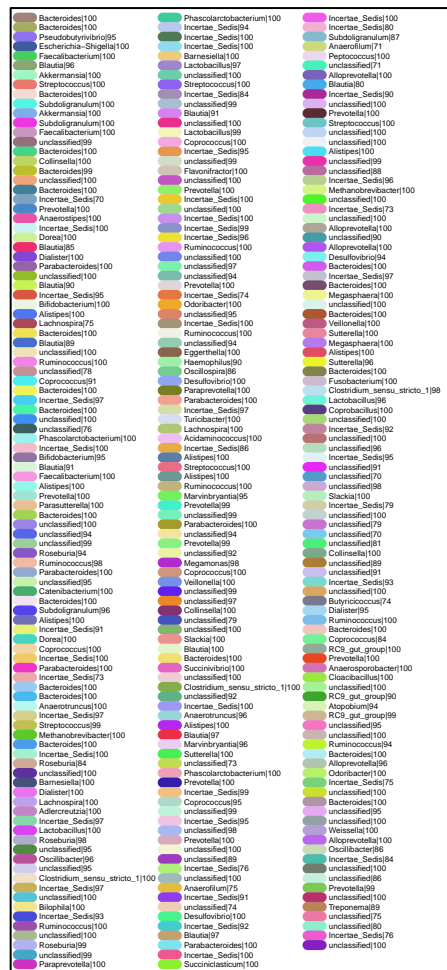


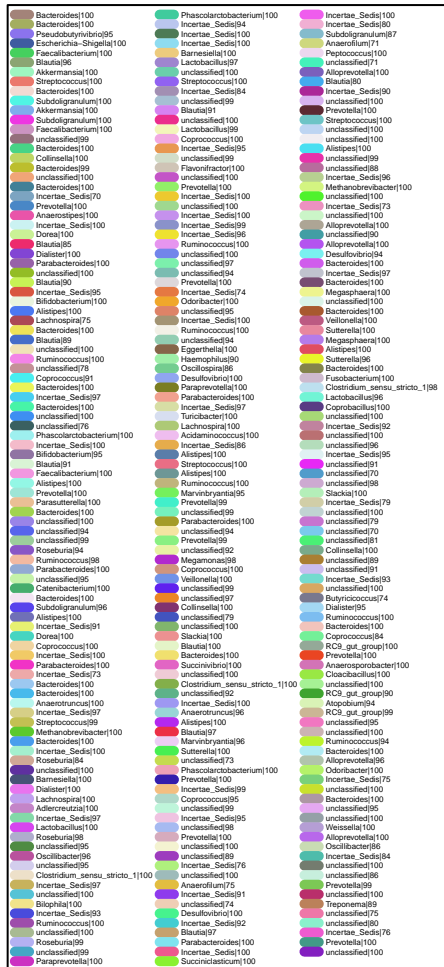
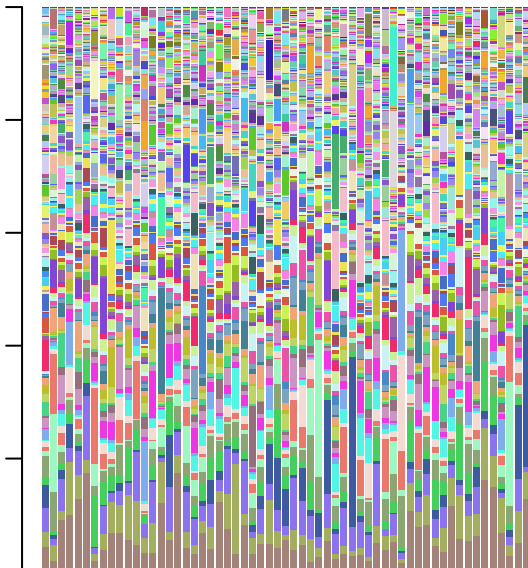
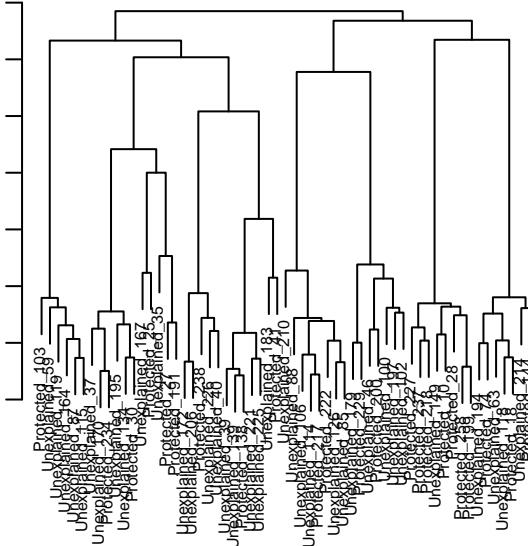
The figure displays a hierarchical clustering analysis of 150 samples based on 1000 SNPs. The dendrogram on the left illustrates the hierarchical relationship between samples, with labels for Protected and Unexplained components. The heatmap on the right shows the expression levels of the 1000 SNPs for each sample, with a color scale from blue (low) to red (high).

The dendrogram labels include:

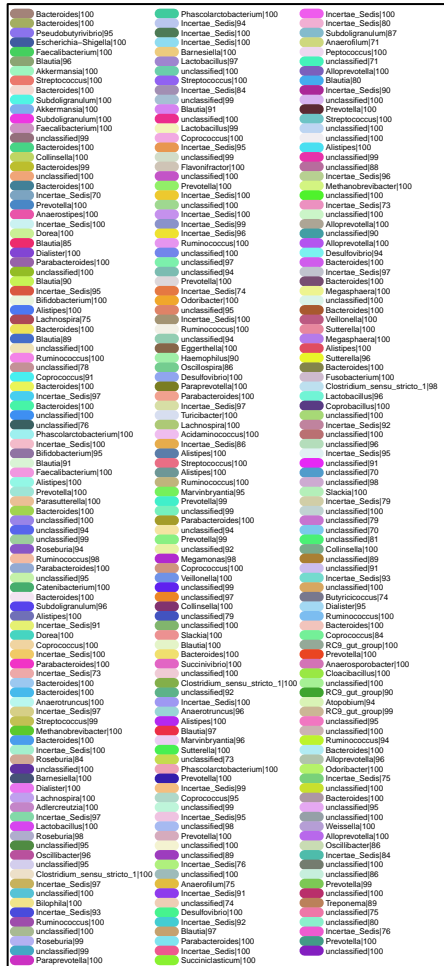
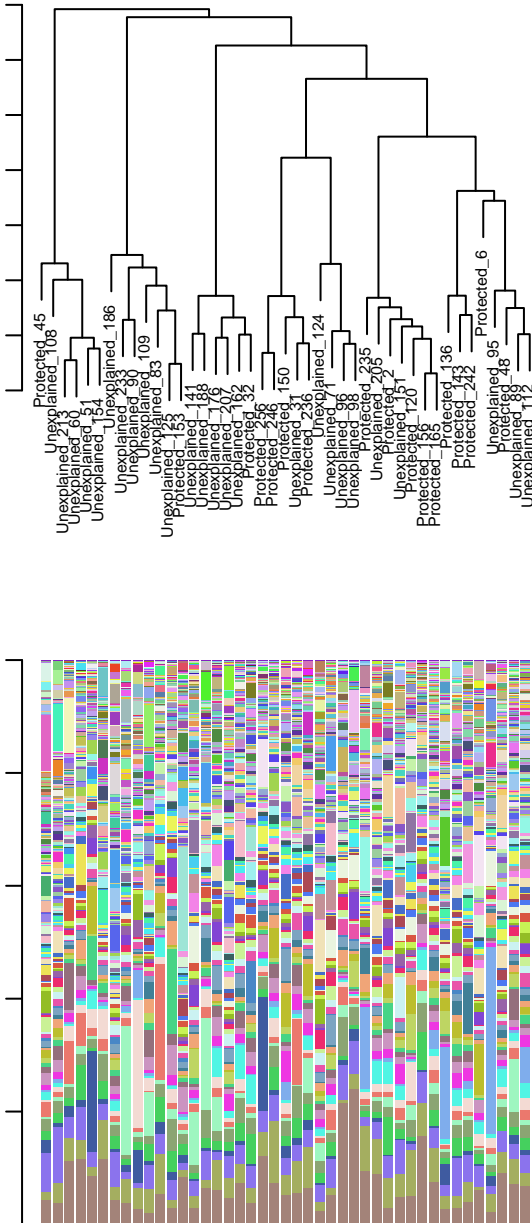
- Protected\_117
- Unexplained\_128
- Protected\_54
- Unexplained\_64
- Protected\_230
- Protected\_232
- Protected\_174
- Unexplained\_145
- Protected\_55
- Protected\_101
- Unexplained\_175
- Unexplained\_131
- Protected\_231
- Protected\_77
- Unexplained\_57
- Unexplained\_75



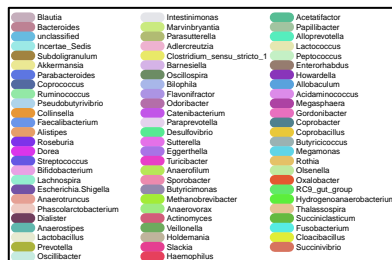
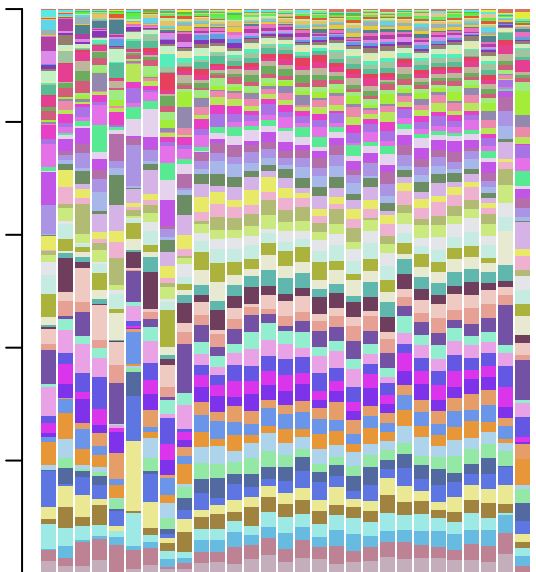
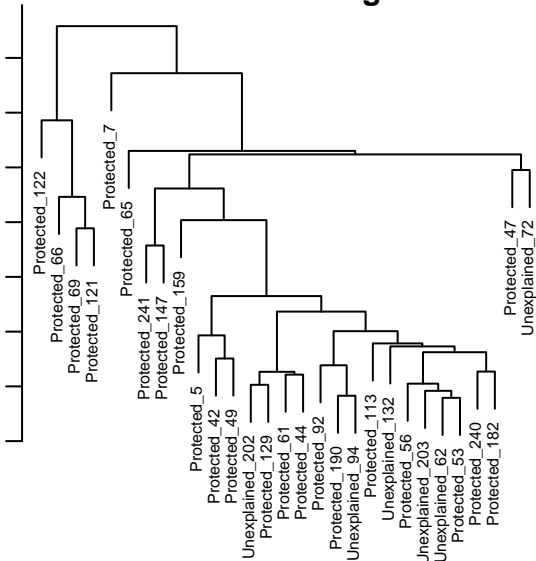
# Cluster Dendrogram



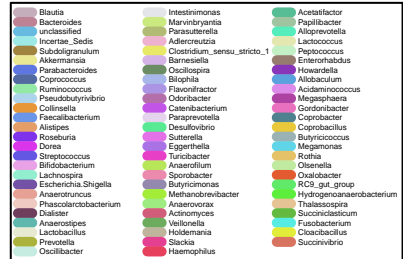
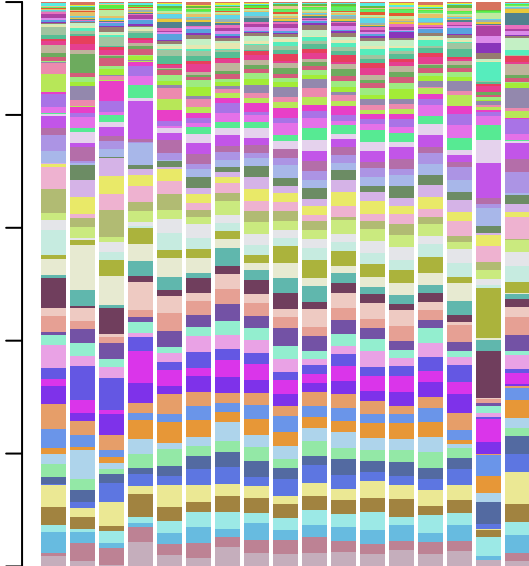
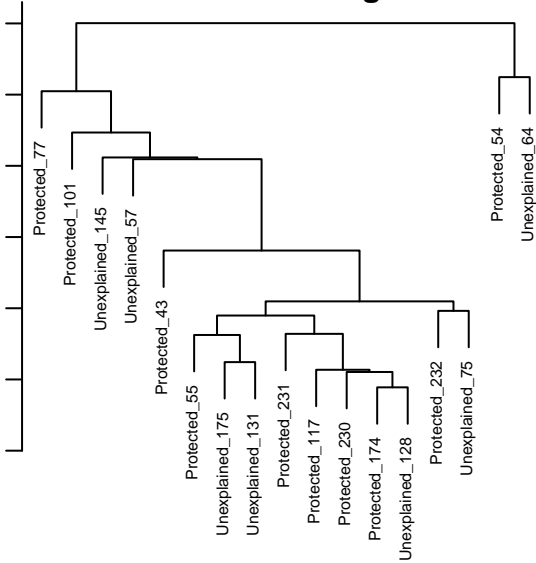
# Cluster Dendrogram



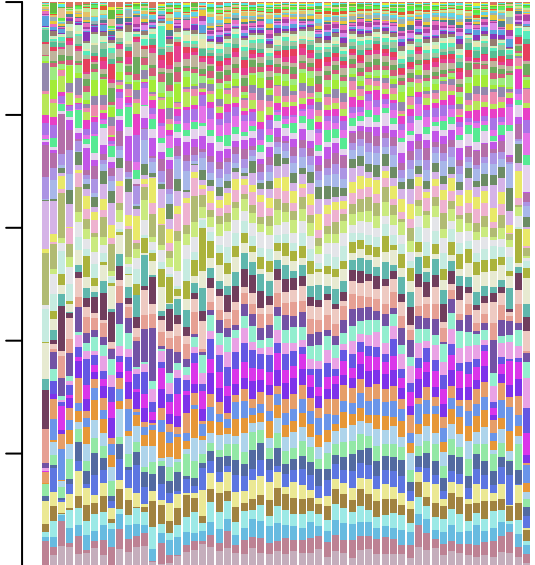
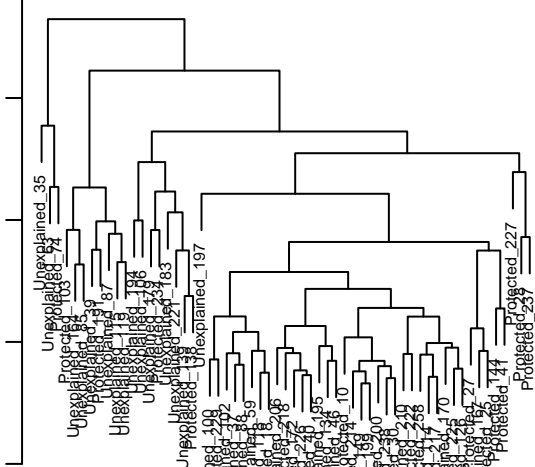
## Cluster Dendrogram



# Cluster Dendrogram

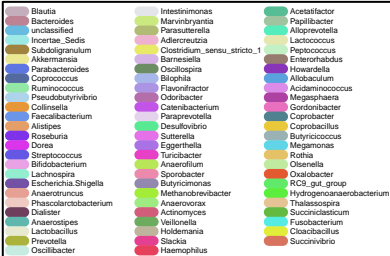
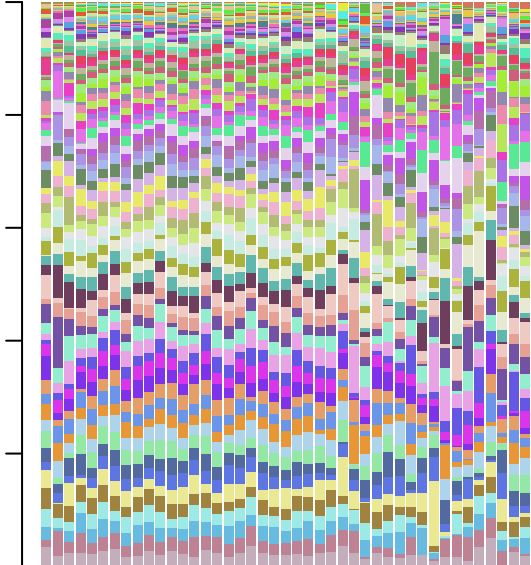
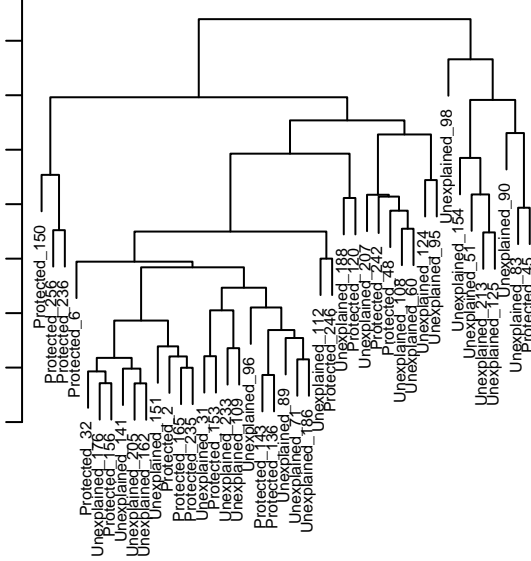


# Cluster Dendrogram



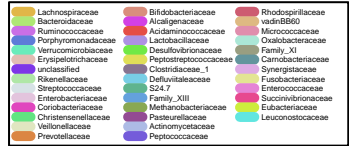
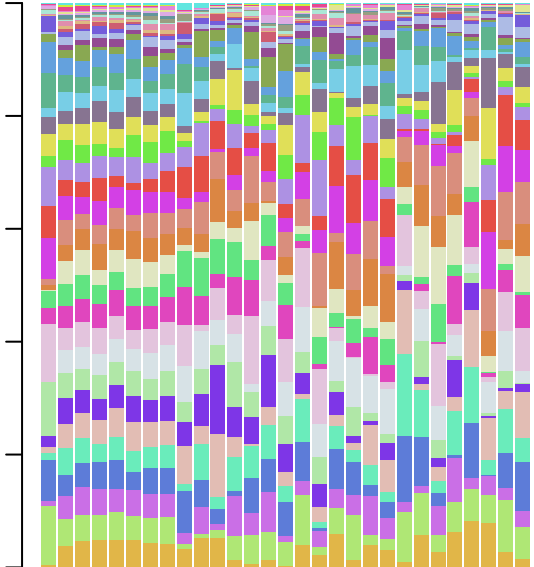
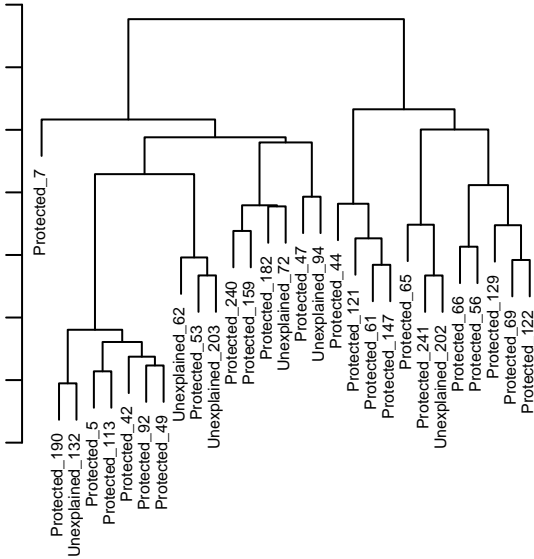
- |                       |                              |                          |
|-----------------------|------------------------------|--------------------------|
| Blautia               | Intestinimonas               | Aceabacter               |
| Bacteroides           | Marvinbryantia               | Papillibacter            |
| Unclassified          | Parasuterella                | Altipontella             |
| Incertae_Sedis        | Adlercreutzia                | Lactococcus              |
| Subdoligranulum       | Clostridium_serasu_stricto_1 | Pectococcus              |
| Akkermansia           | Barnesiella                  | Enterorhabdus            |
| Parabacteroides       | Oscillospira                 | Howardella               |
| Coprococcus           | Blautia                      | Allobaculum              |
| Ruminococcus          | Flavonifractor               | Acidaminococcus          |
| Pseudobutyribacter    | Oribacter                    | Megaphasma               |
| Catenibacterium       | Catenibacterium              | Gordonibacter            |
| Fasclibacterium       | Paraprevotella               | Cuprobacter              |
| Altipontella          | Desulfotribrio               | Coprobacter              |
| Roseburia             | Sutterella                   | Butyrivibrio             |
| Dorea                 | Eggerthella                  | Megamonas                |
| Streptococcus         | Turicibacter                 | Rothia                   |
| Bifidobacterium       | Anaerostipes                 | Olsenella                |
| Lactobacillus         | Sporobacter                  | Oxalobacter              |
| Escherichia_Shigella  | Butyrivibrio                 | RC9_gut_group            |
| Anaerotruncus         | Methanobrevibacter           | Hydrogenosymbiobacterium |
| Phascolarctobacterium | Anaerovorax                  | Thalassospora            |
| Dialister             | Actinomyces                  | Succinobacterium         |
| Lactobacillus         | Velloneia                    | Fusobacterium            |
| Prevotella            | Holdemania                   | Cloacibacterium          |
| Oscillospira          | Haemophilus                  | Succinobacterium         |

# Cluster Dendrogram

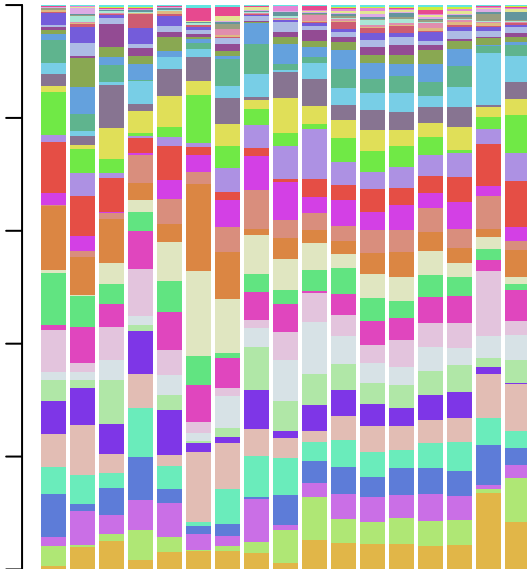
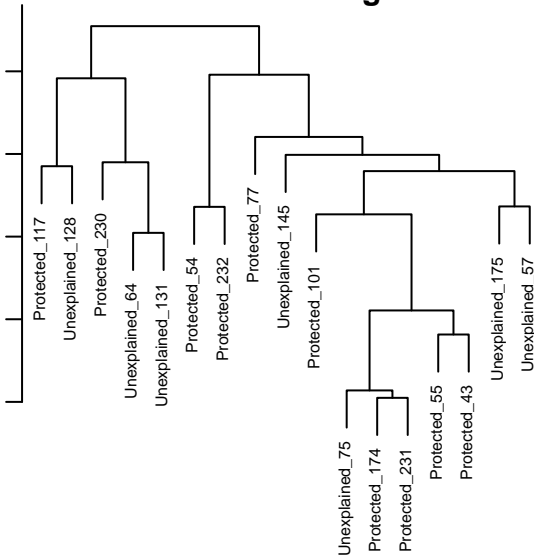




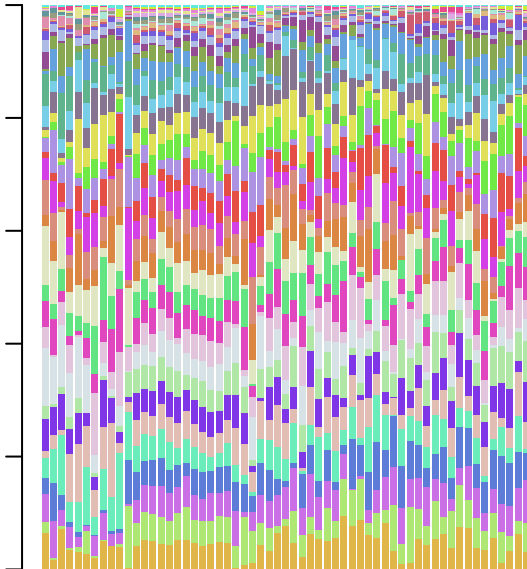
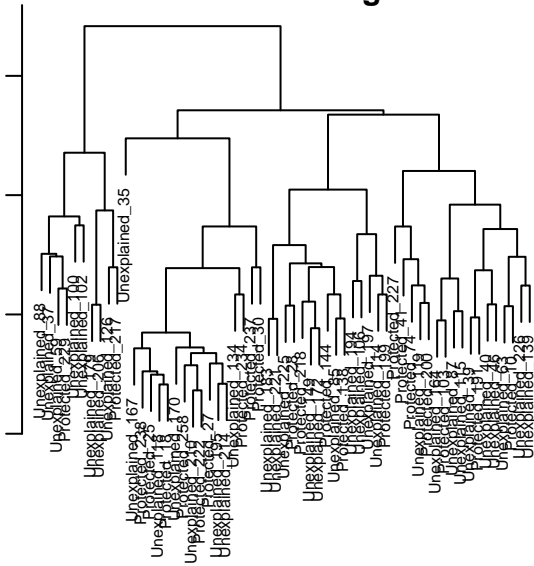
# Cluster Dendrogram



# Cluster Dendrogram



# Cluster Dendrogram



Cluster Dendrogram

