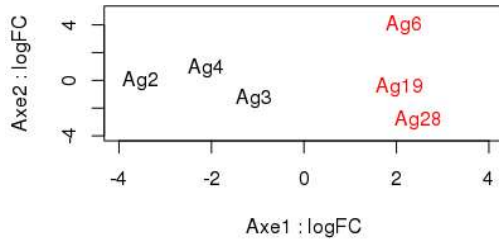
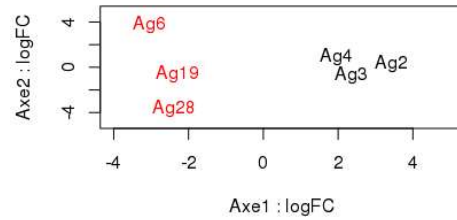


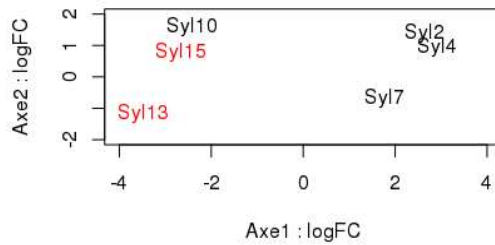
Supplementary figure 2: Plots of samples relations by using multidimensional scaling plot (MDS) from EdgeR. Infected individuals are in red, and non-infected individuals are in black.



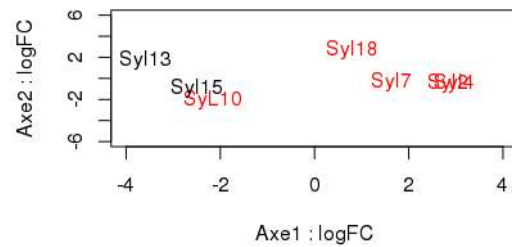
A. MDS plot from *A. gummiferum* using the de novo transcriptome assembly as reference for alignment.



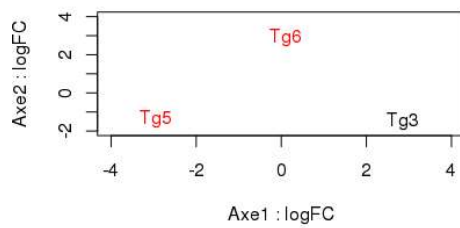
B. MDS plot from *A. gummiferum* using the *E. grandis* genome as reference for alignment.



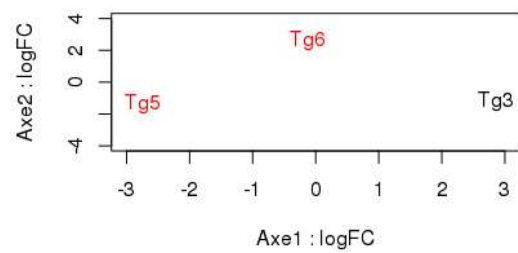
C. MDS plot from *S. longifolium* using the de novo transcriptome assembly for alignment.



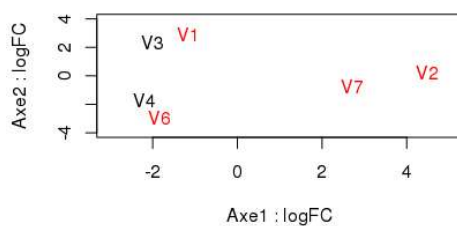
D. MDS plot from *S. longifolium* using the *E. grandis* genome as reference for alignment.



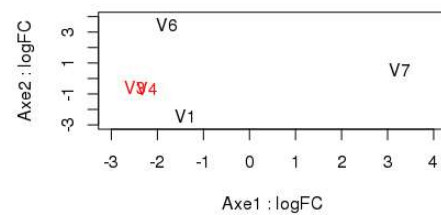
E. MDS plot from *T. glauca*-FAR using the de novo transcriptome assembly for alignment.



F. MDS plot from *T. glauca*-FAR using the *E. grandis* genome as reference for alignment.



G. MDS plot from *T. glauca*-BDS using the de novo transcriptome assembly for alignment.



H. MDS plot from *T. glauca*-BDS using the *E. grandis* genome as reference for alignment.