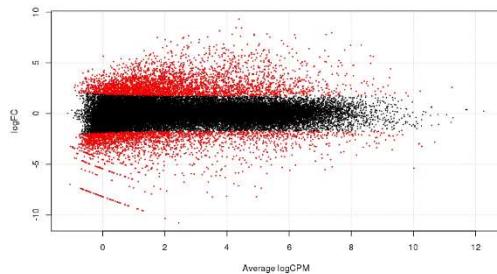
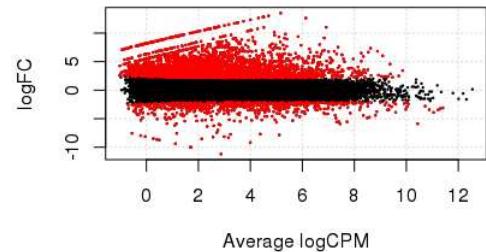


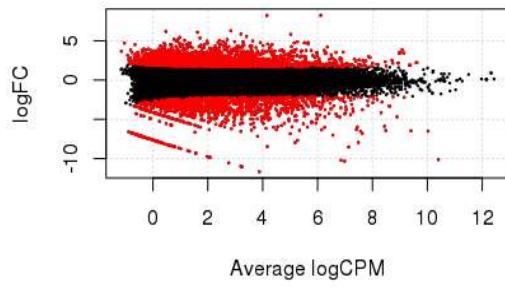
Supplementary figure 1: EdgeR's plotSmear function plots the log-fold change (i.e., the log ratio of normalized expression levels between non-infected and infected) against the log counts per million (CPM).



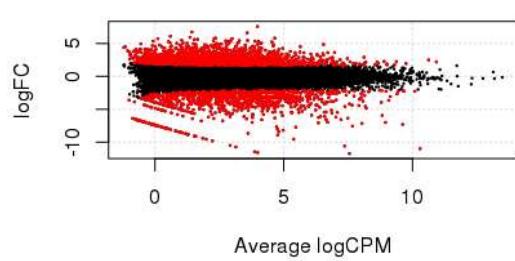
A. PlotSmear from *A. gummiferum* using the de novo transcriptome assembly as reference for alignment.



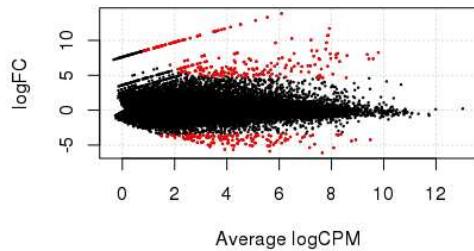
B. PlotSmear from *A. gummiferum* using the *E. grandis* genome as reference for alignment.



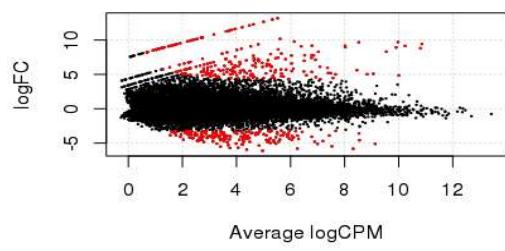
C. PlotSmear from *S. longifolium* using the de novo transcriptome assembly for alignment.



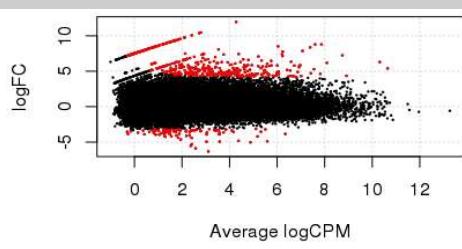
D. PlotSmear from *S. longifolium* using the *E. grandis* genome as reference for alignment.



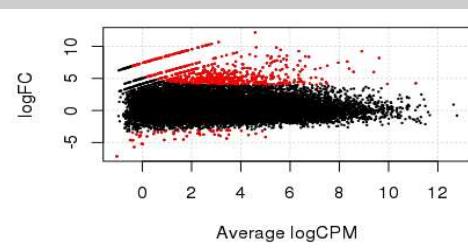
E. PlotSmear from *T. glauca*-FAR using the de novo transcriptome assembly for alignment.



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



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



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