Figure S15: miRbiom: The above tool to discover the miRNA profile without any need of sRNA-sequencing data has been implemented here as a software server. User needs to profie the RNA-seq data for any given condition. This data is run through the miRNA biogenesis models implemented through RBP:miRNA conditional networks based implementation of XGBoost regression, which generates a relative regression score for various miRNAs capturing the potential expression profile of miRNAs for the given condition. It generates a plot of expression profiles of various miRNAs in interactive fashion. Selections can be made here to study the miRNA targets for their functional enrichment as well as pathways analysis. miRNA target information from various databases like miRTarbase etc has been provided. Provisions have also been made to map the miRNA targets in collective fashion and view them in KEGG pathways maps.