



Fig 1. Visualization of the same GTEx data as in Figure 1 (a) across all tissues using standard and widely used approaches - Principal Component Analysis (PCA), Multi dimensional Scaling (MDS), t-SNE and hierarchical clustering. All the analysis are done on log CPM normalized expression data to remove library size effects. **(a)**: Plot of PC1 vs PC2 on the log CPM expression data, **(b)**: Plot of first two dimensions of the t-SNE plot, **(c)** Plot of first two dimensions of the Multi-Dimensional Scaling (MDS) plot. **(d)** Dendrogram for the hierarchical clustering of the GTEx tissue samples based on the log CPM expression data.