



Figure 7. Comparison between rat and human tissues. **A** Dendrogram based on limma batch corrected $\log_{10}(\text{nTPM} + 1)$ values of ortholog genes of compared tissues based on sample to sample spearman distance. Dendrogram clustering calculated throughUPGMA (unweighted pair group method with arithmetic mean). **B** UMAP dimensionality reduction plot based on limma batch corrected $\log_{10}(\text{nTPM} + 1)$ values. **C** Results of the hypergeometric test assessing overlap of tissue elevated ortholog genes between all rat against all human comparison tissues. See method sections for details on the calculation. **D** Alluvial plot depicting the overlap of tissue specificity categorization between rat and human orthologs. Categorization was calculated at this comparison tissue hierarchy.