Dimensionality reduction by UMAP reinforces sample heterogeneity analysis in bulk transcriptomic data - Supplementary

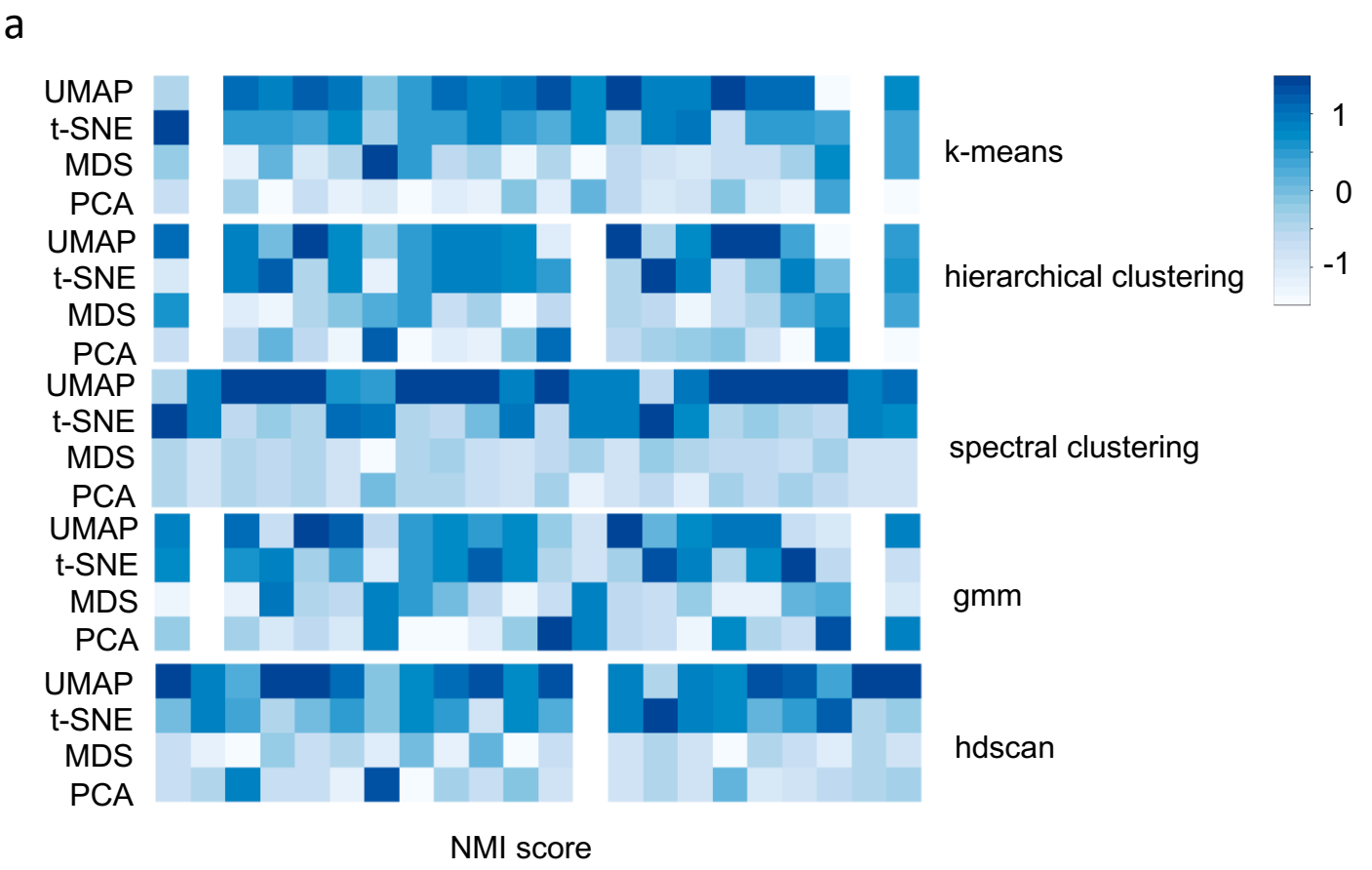
Table S2: Dimensionality reduction methods, 4 methods

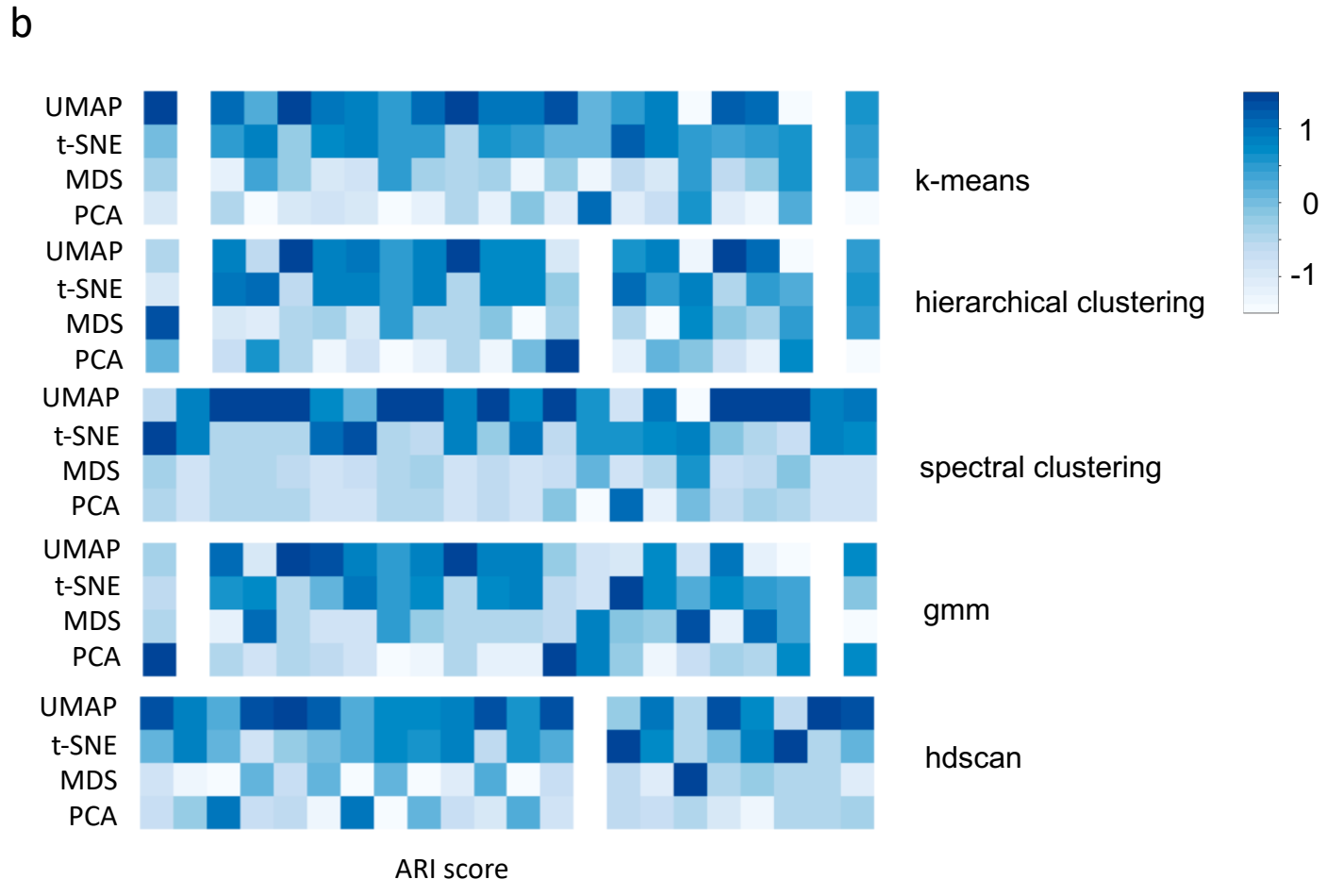
Algorithm	Version	Availability	Implementation language	Parameter
UMAP	0.3.10	https://github.com/lmcinnes/umap/	Python	n_components=2, n_neighbors=15, min_dist=0.1, metric='euclidean'
t-SNE	scikit-learn 0.23.1	https://scikit-learn.org/	Python	*n_components=2, perplexity=30.0, metric='euclidean', early_exaggeration=12.0, learning_rate=200.0, n_iter=1000,*
MDS	scikit-learn 0.23.1	https://scikit-learn.org/	Python	*n_components=2, *, metric=True, n_init=4, max_iter=300, verbose=0, eps=0.001, n_jobs=None, random_state=None, dissimilarity='euclidean'*
PCA	scikit-learn 0.23.1	https://scikit-learn.org/	Python	*n_components=2, copy=True, whiten=False, svd_solver='auto', tol=0.0, iterated_power='auto', random_state=None*

Table S3: 5 clustering algorithms

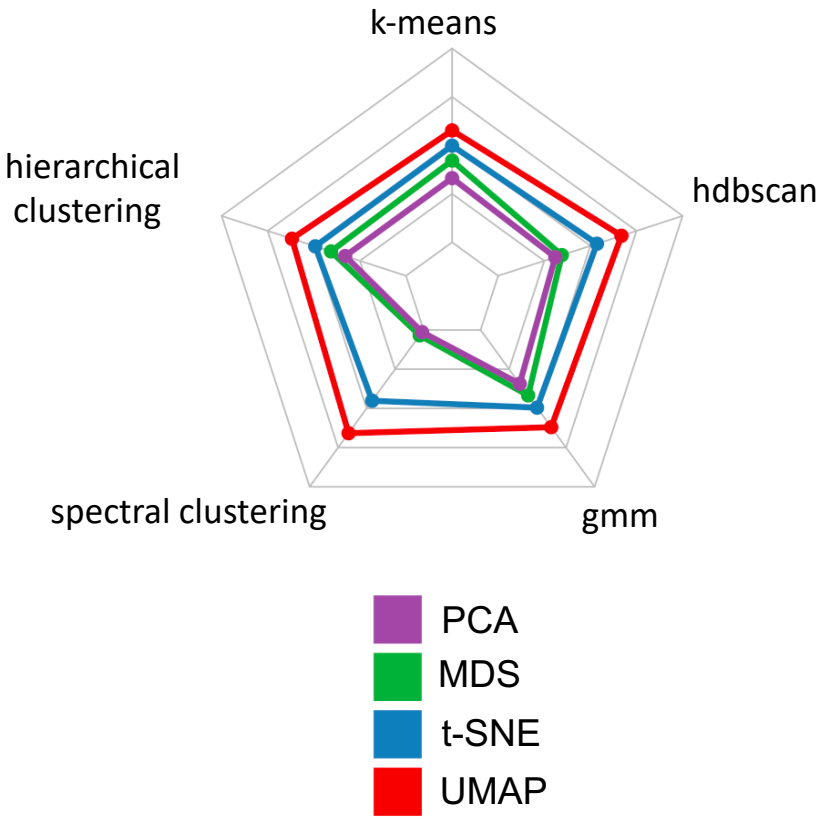
Algorithm	Version	Availability	Implementation language
k-means	scikit-learn 0.23.1: sklearn.cluster.KMeans	https://scikit-learn.org/	Python
Hierarchical clustering	scikit-learn 0.23.1: sklearn.cluster.AgglomerativeClustering	https://scikit-learn.org/	Python
Spectral clustering	scikit-learn 0.23.1: sklearn.cluster.SpectralClustering	https://scikit-learn.org/	Python
gmm	scikit-learn 0.23.1: sklearn.mixture.GaussianMixture	https://scikit-learn.org/	Python
hdbscan	hdbscan 0.8.18	https://hdbscan.readthedocs.io/	Python

Figure S1: Clustering accuracy of five clustering algorithms on embedded space by four dimensionality reduction methods



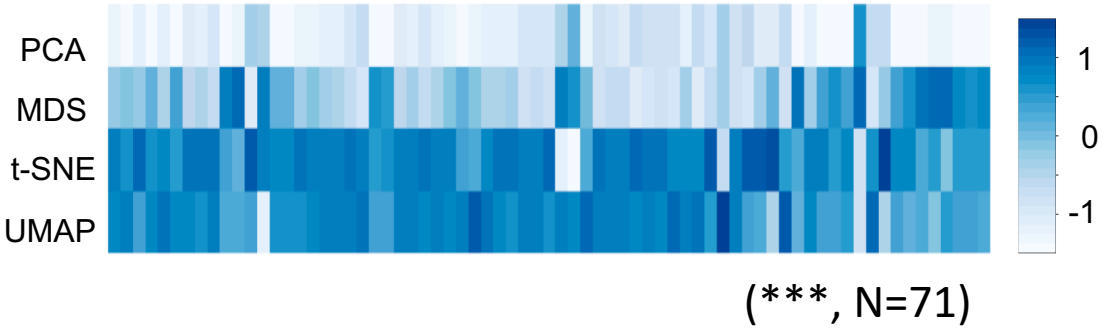


c



a. Heatmap for clustering accuracy by normalized mutual information (NMI). Darker blue means higher clustering accuracy. Five clustering algorithms are listed on the right side. [“1” in the heatmap represent the perfect accuracy, “0”…. “-1” represent….]
b. Heatmap for clustering accuracy by adjusted Rand index (ARI).
c. Radar plot of clustering accuracy (ARI score) comparison using five clustering methods. The average ARI score was on 22 datasets with cluster labels. The input was the embedded two-dimensional coordinates of each dimensionality reduction methods. Larger scale denotes better clustering accuracy, and UMAP outperformed the other three.

Figure S2: Neighborhood preserving (knn_k = 30), Average Jaccard index with 30 neighborhoods.



Heatmap for evaluating neighbourhood preserving of each method on 71 datasets. The number of neighbours is set as 30. The darker the colour is, the better the local information is retained.

Figure S3: Visualization of dataset GSE98793 and GSE107990 showing batch effects in two-dimensional space by dimensionality reduction methods.

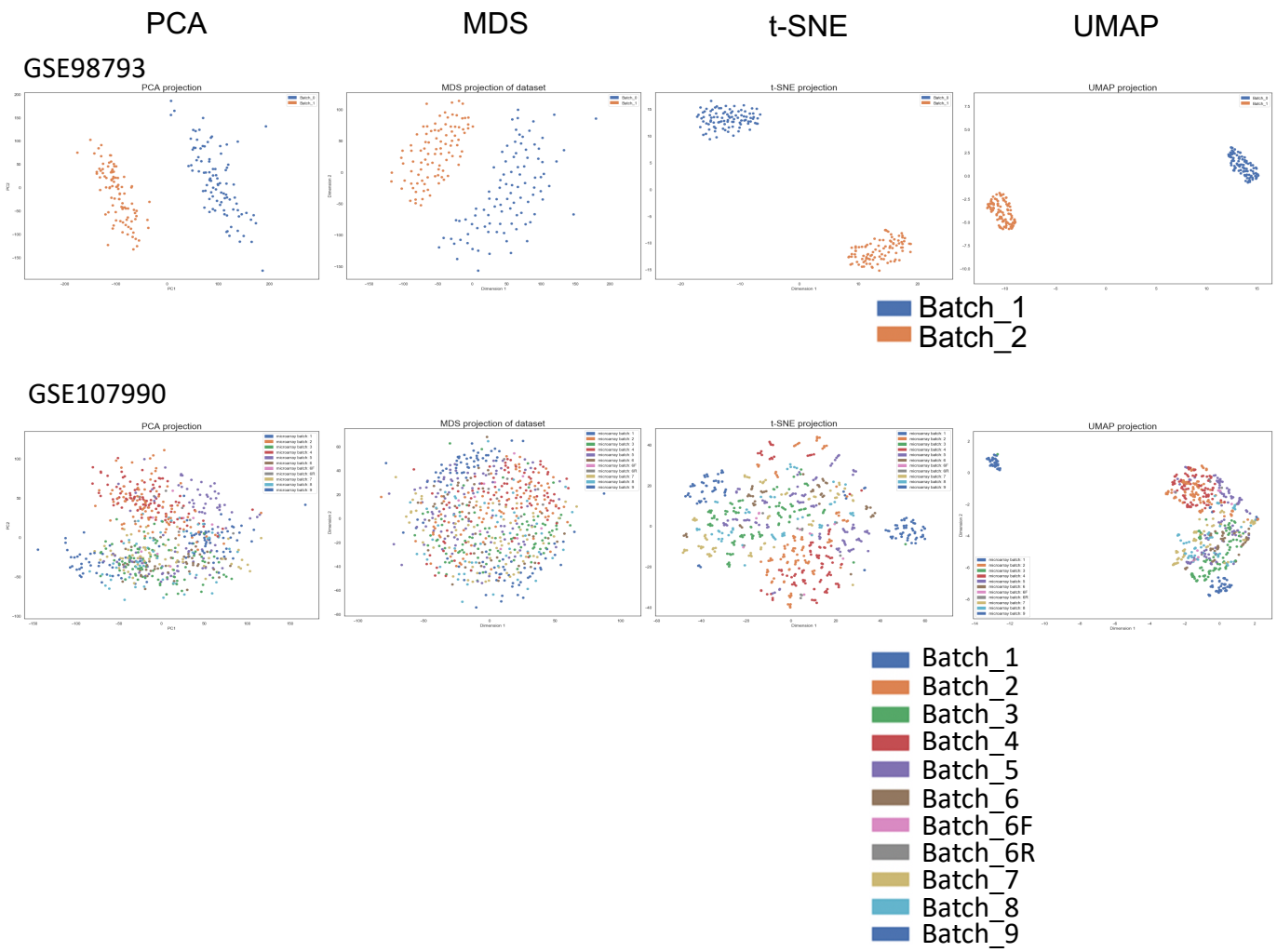
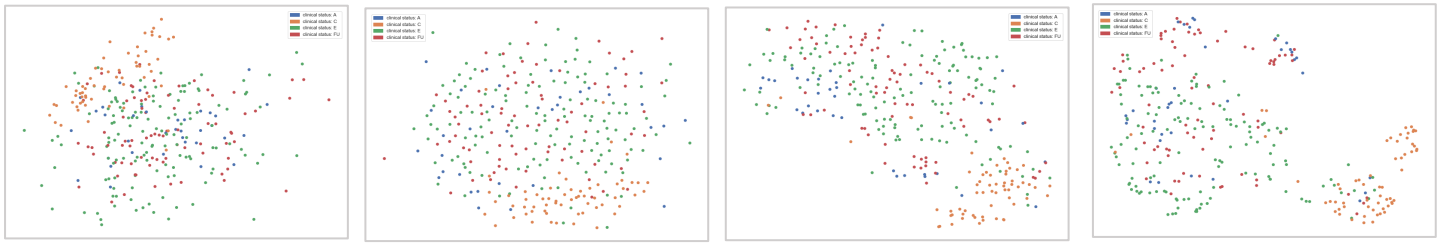


Figure S4: Visualization of eight datasets illustrating biological groups by dimensionality reduction methods. Colours represents groups.

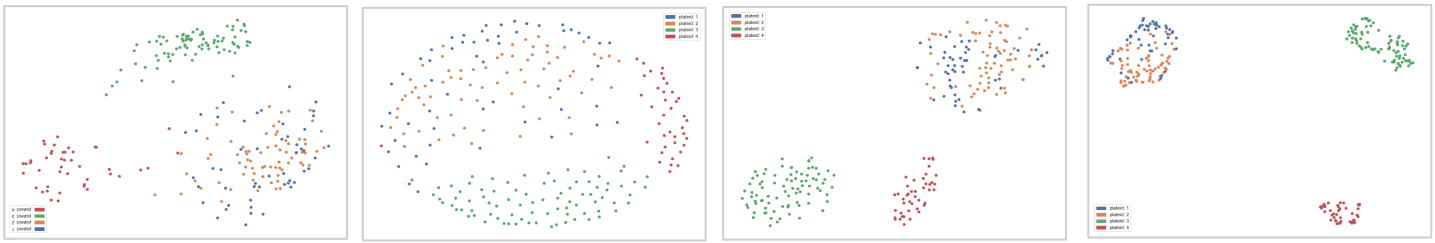
PCA MDS t-SNE UMAP

GSE35007



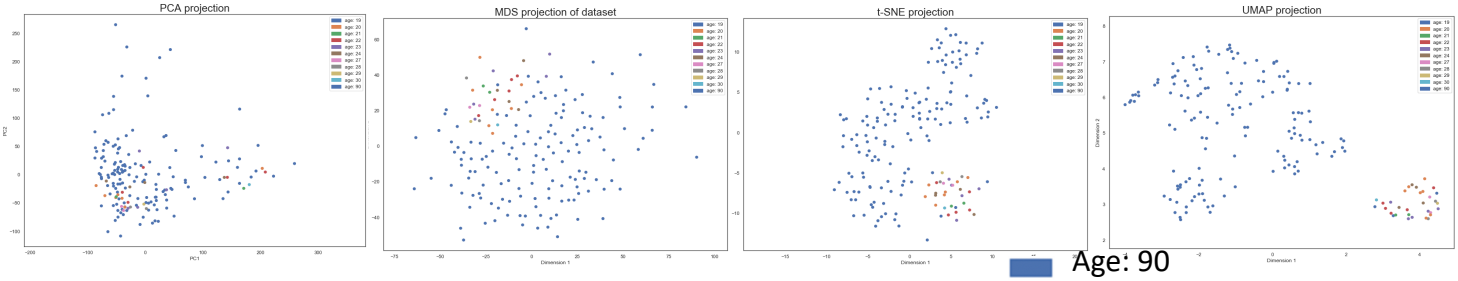
Clinical status: A
Clinical status: C
Clinical status: E
Clinical status: FU

GSE58137



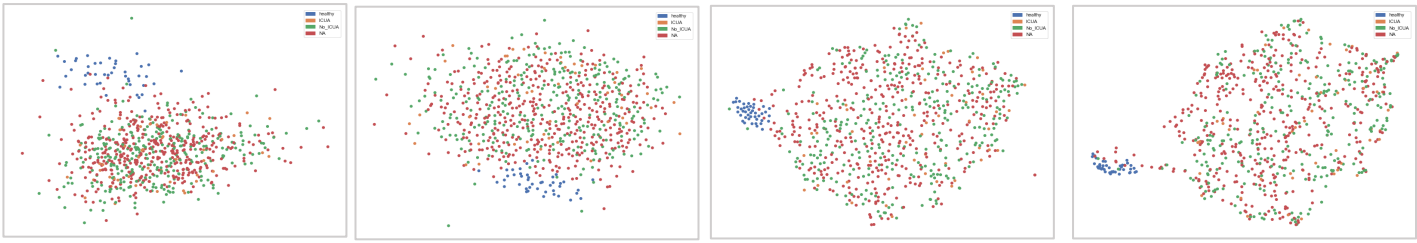
Plateid: 1
Plateid: 2
Plateid: 3
Plateid: 4

GSE65219



Age: 90
Age: others

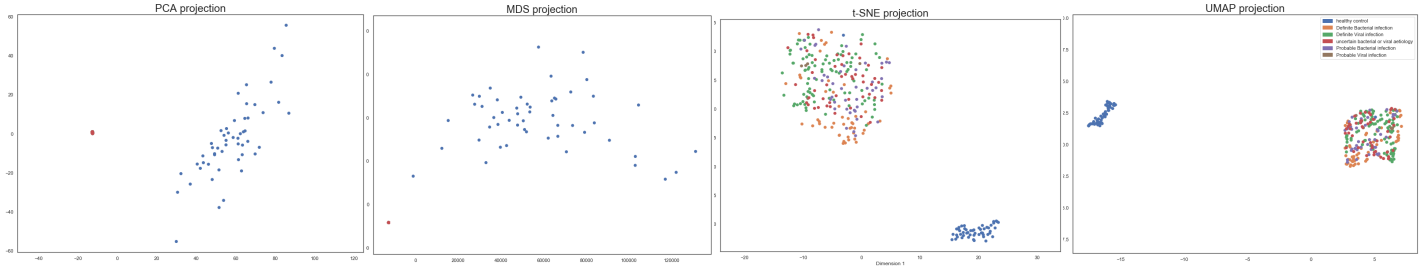
GSE65682



Healthy
ICUA
No ICUA
NA

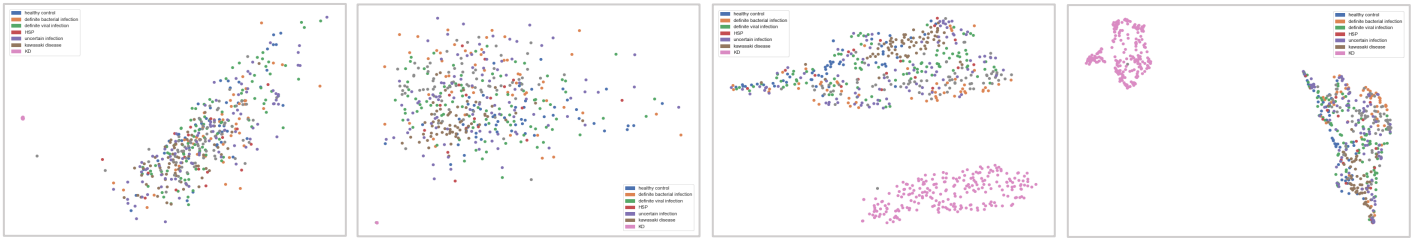
PCA MDS t-SNE UMAP

GSE72809



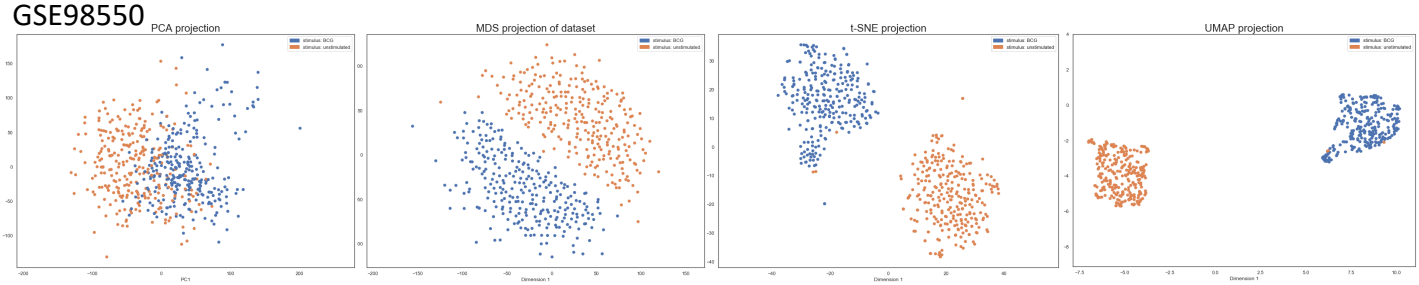
Healthy control
Definite bacterial infection
Definite viral infection
Uncertain bacterial or viral infection
Probable bacterial infection
Probable viral infection

GSE73464



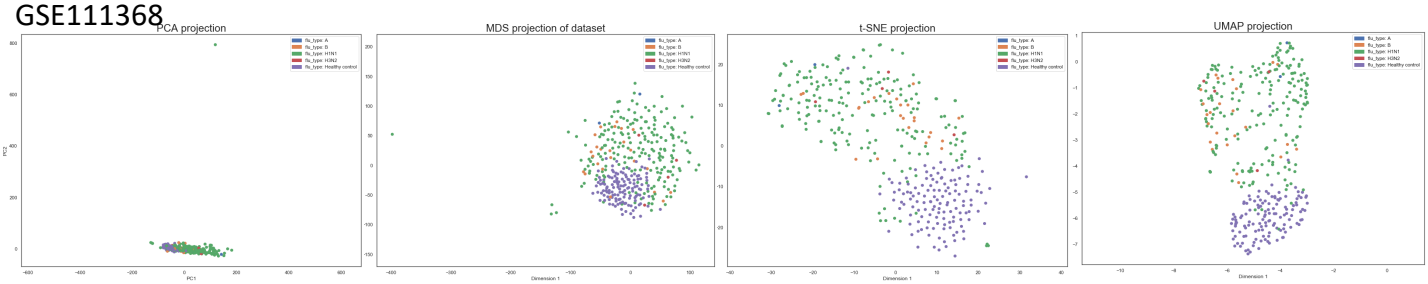
Healthy control
Definite bacterial infection
Definite viral infection
HSP
Uncertain infection
Kawasaki infection
KD

GSE98550



Stimulus: BCG
Stimulus: unstimulated

GSE111368

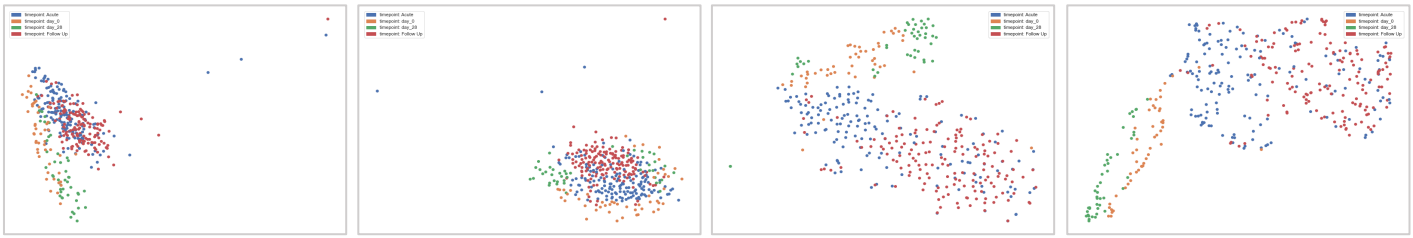


Flu_type: A
Flu_type: B
Flu_type: H1N1
Flu_type: H3N2
Flu_type: healthy control

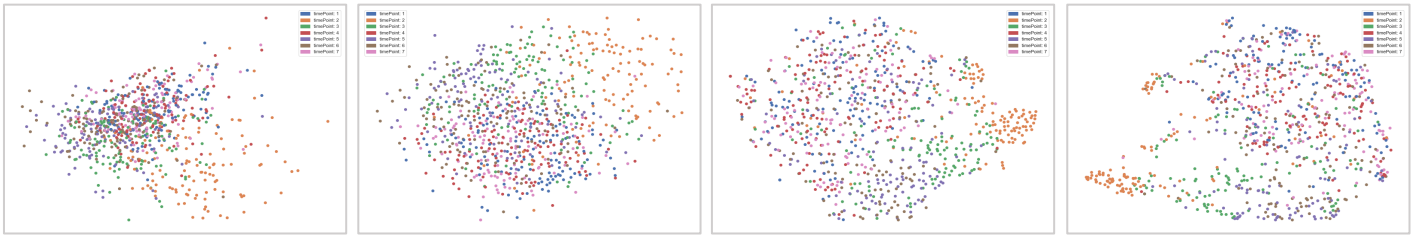
Figure S5: Associating sample features to clustering structure

PCA MDS t-SNE UMAP

GSE61821



GSE68310



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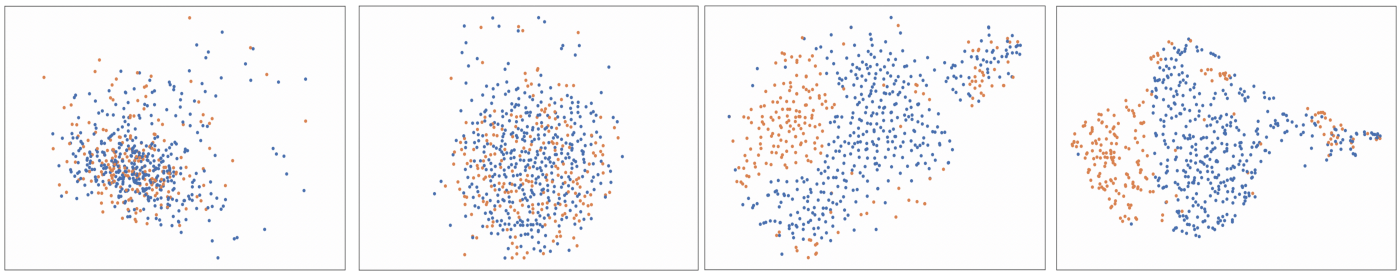

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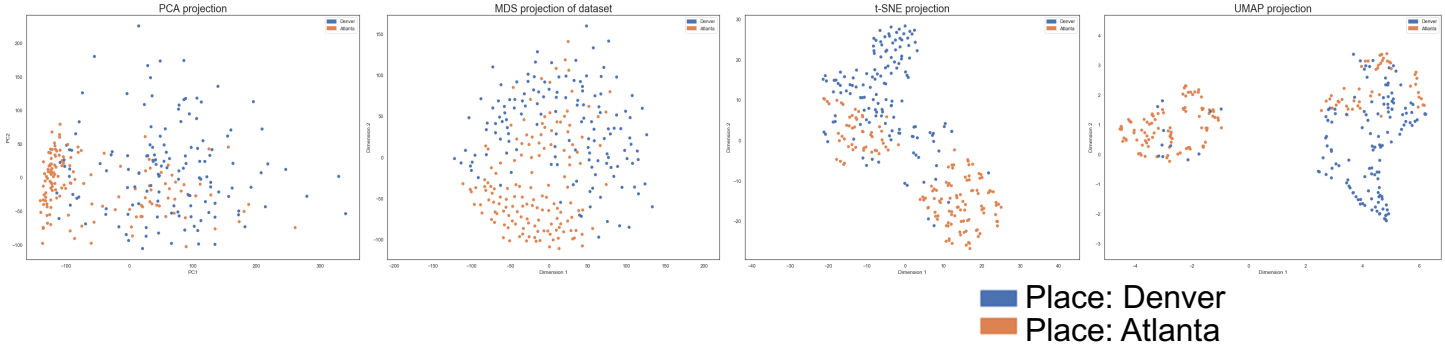
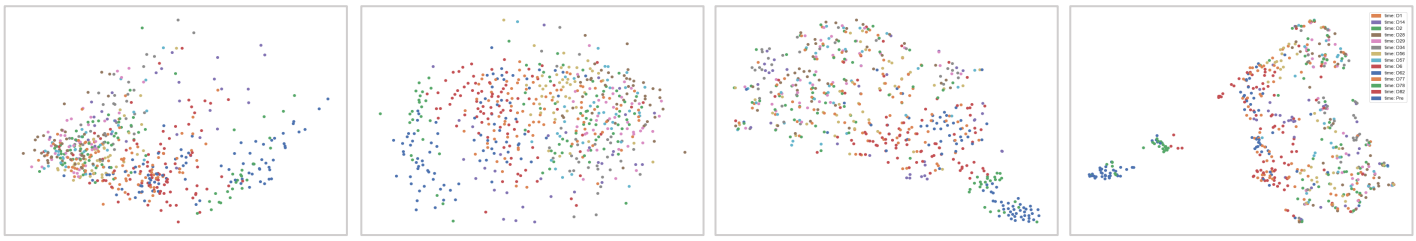
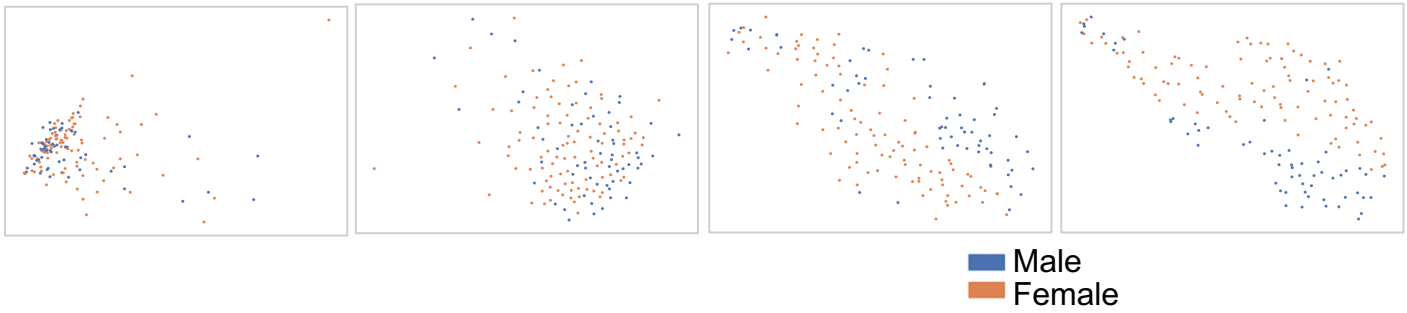


GSE89292: distinct colours for days



PCA MDS t-SNE UMAP

GSE110551



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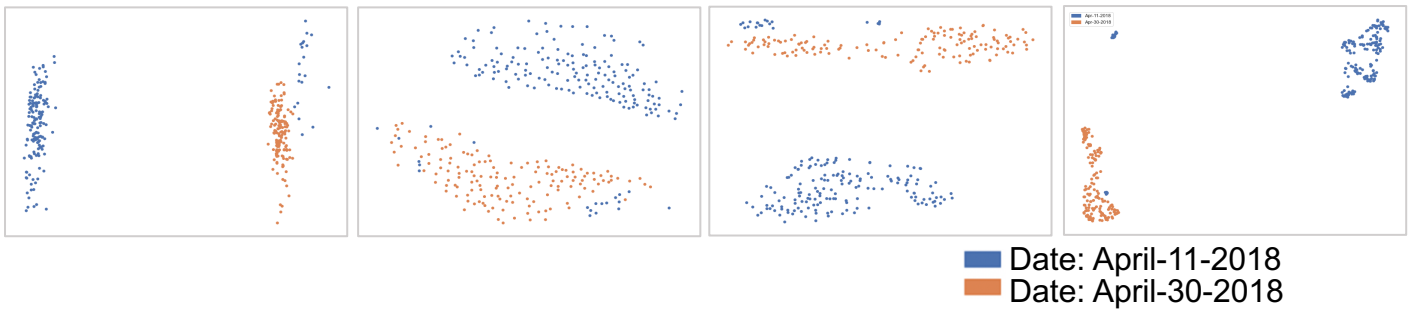

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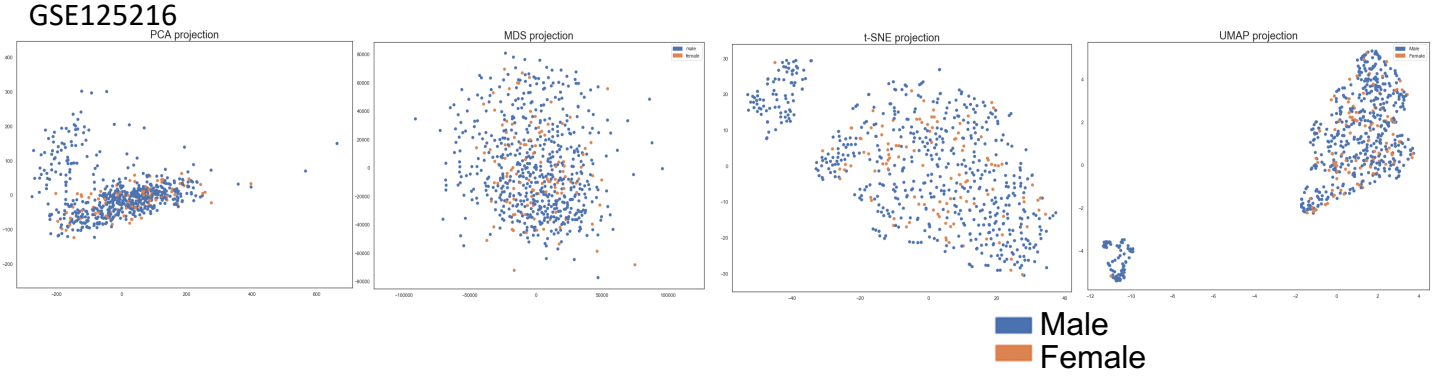


GSE133822

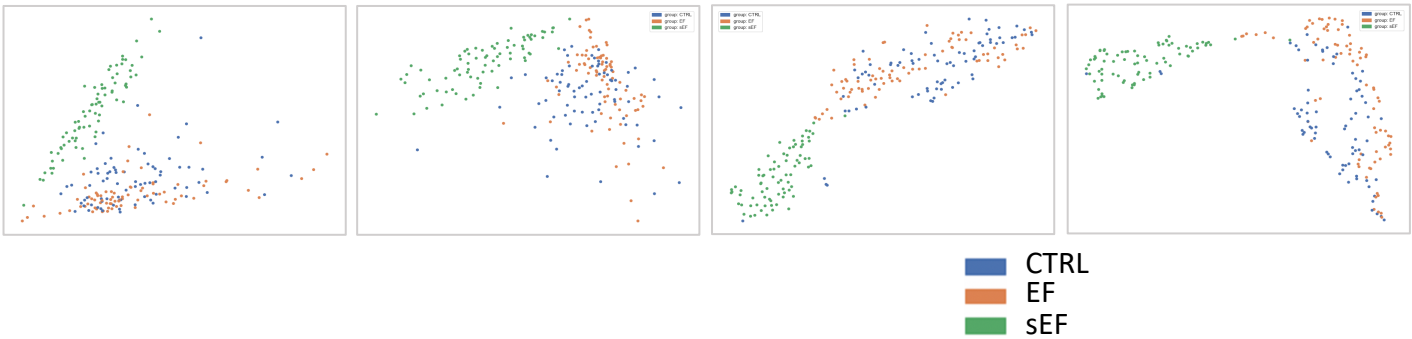
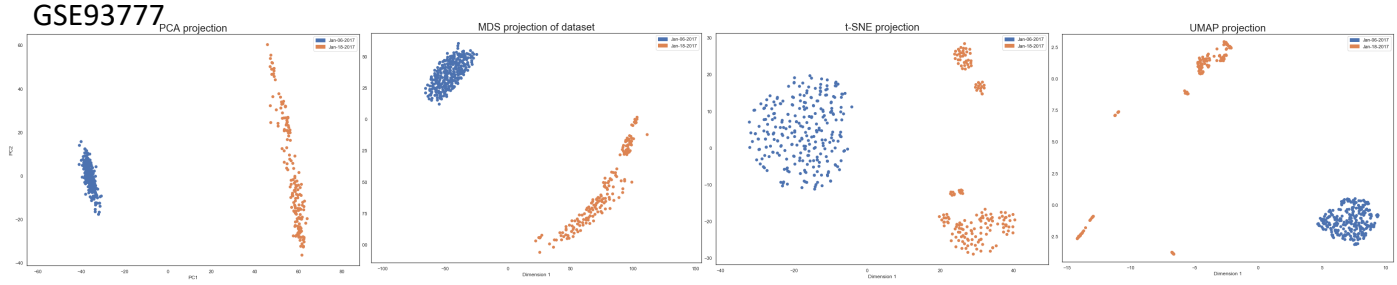


Figure S6: Visualization of datasets showing clustering structures associated no pre-defined features

PCA MDS t-SNE UMAP

GSE93777



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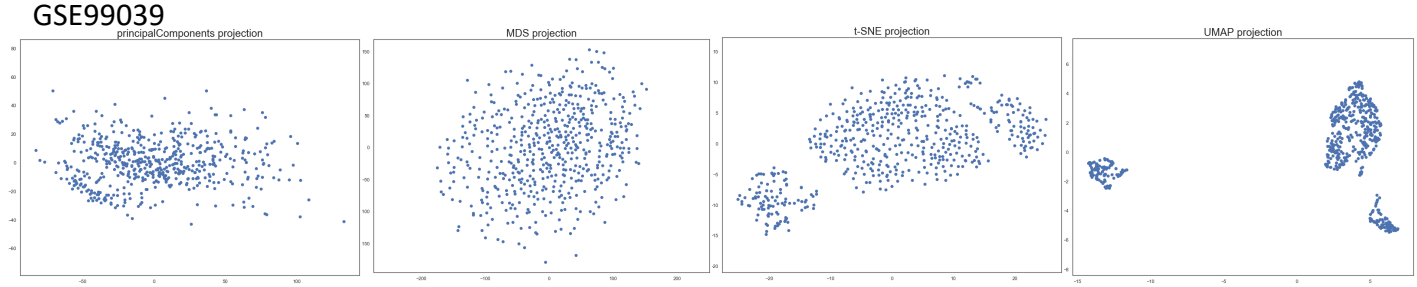
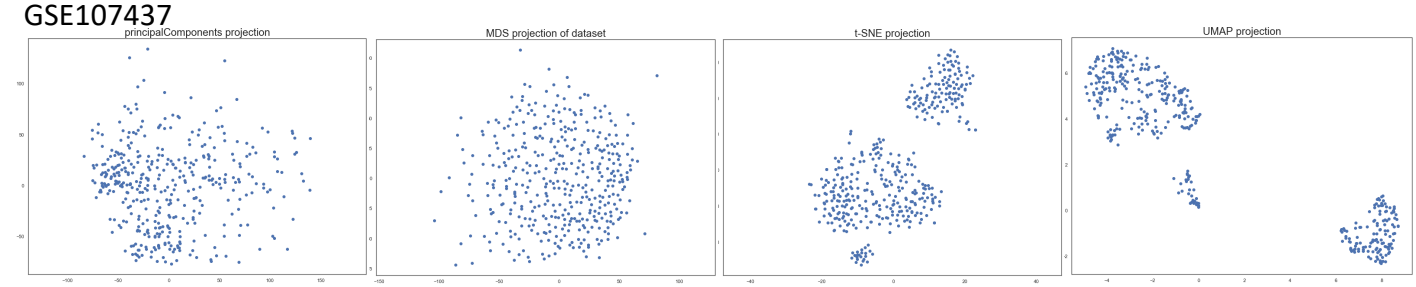


GSE107437



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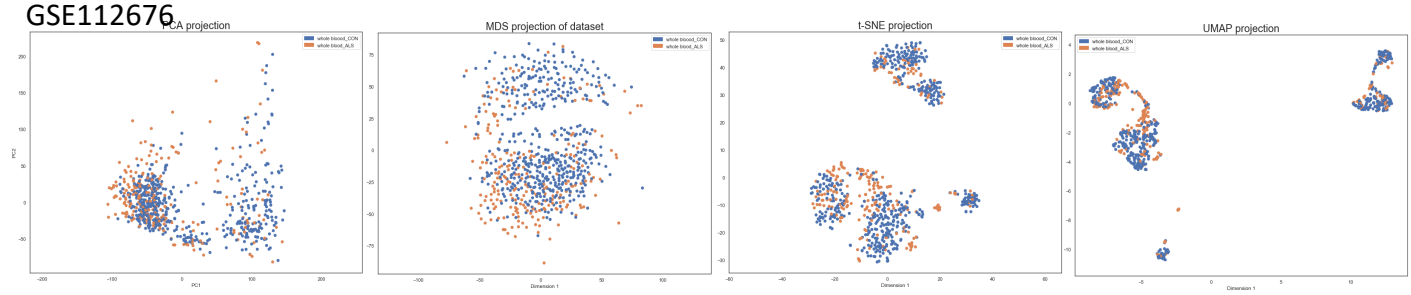
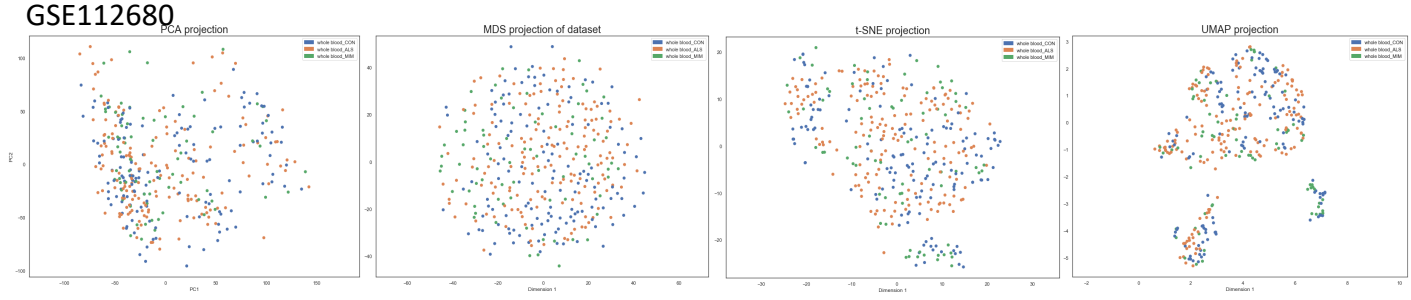


GSE112680



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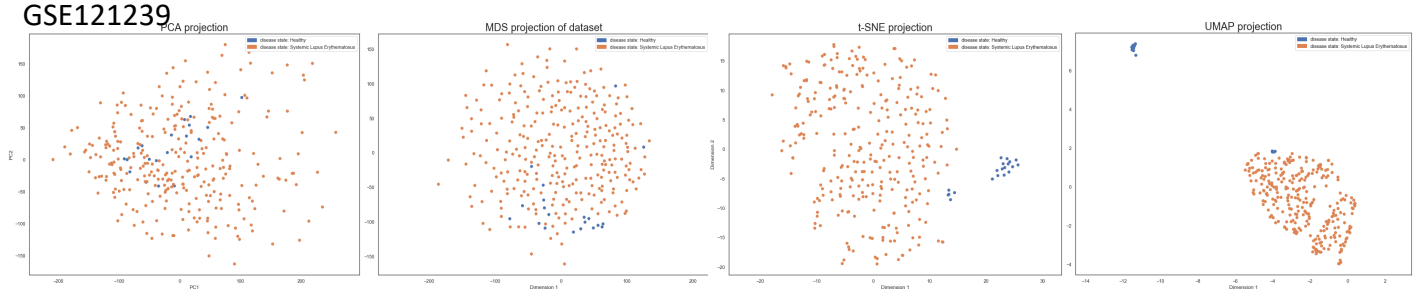
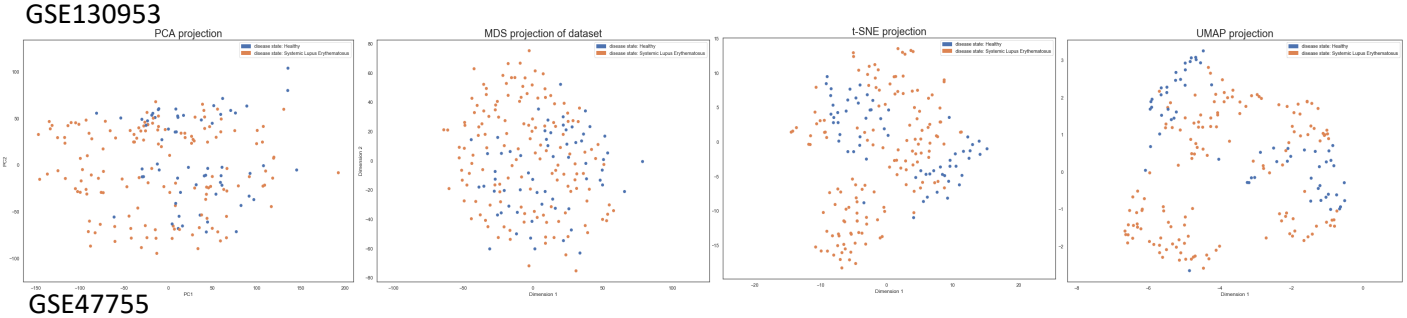
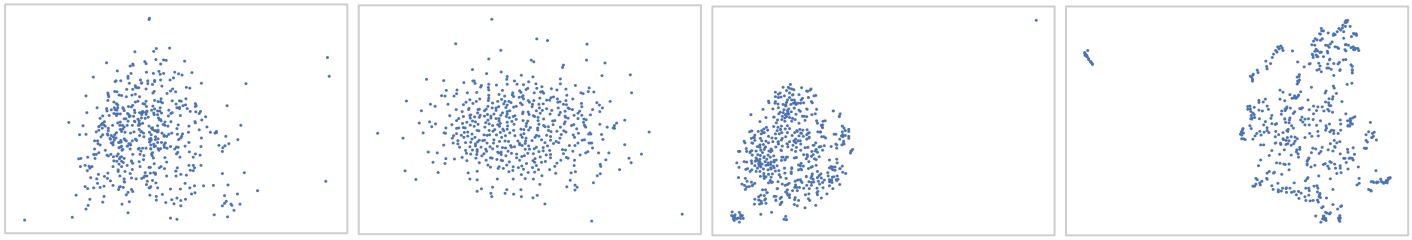


PCA MDS t-SNE UMAP

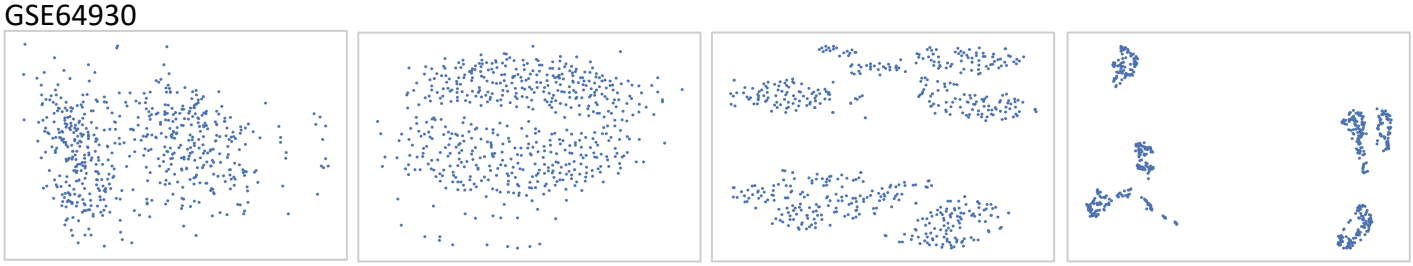
GSE130953



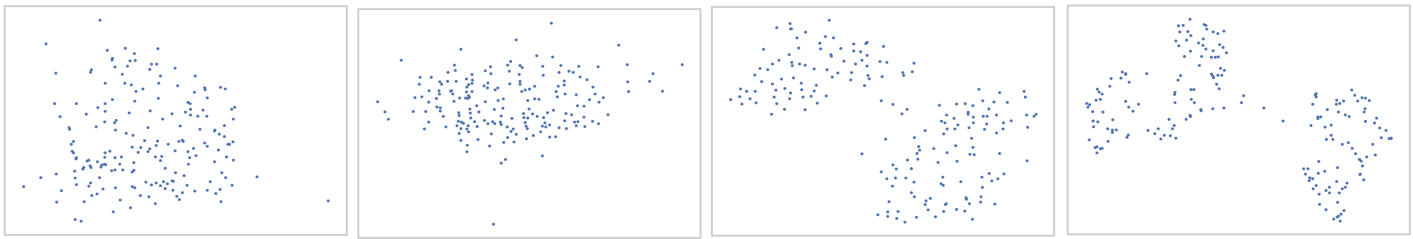
GSE47755



GSE64930



GSE85531



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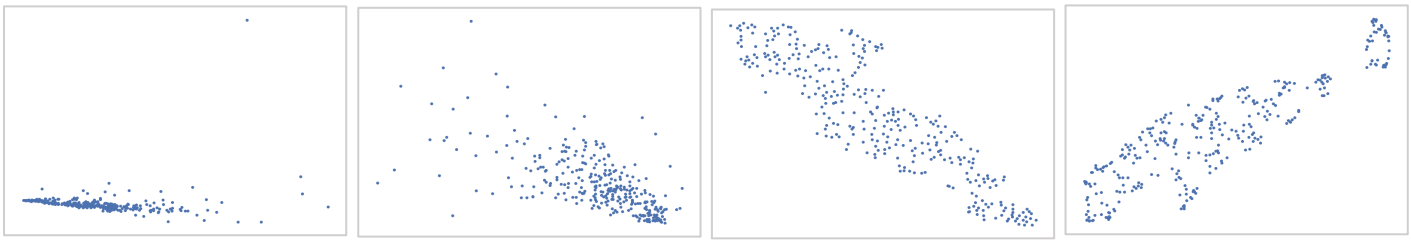
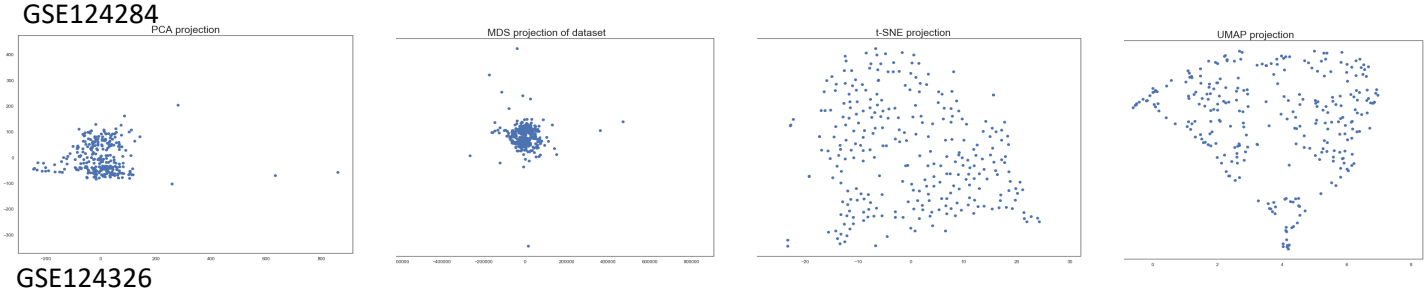


GSE124284



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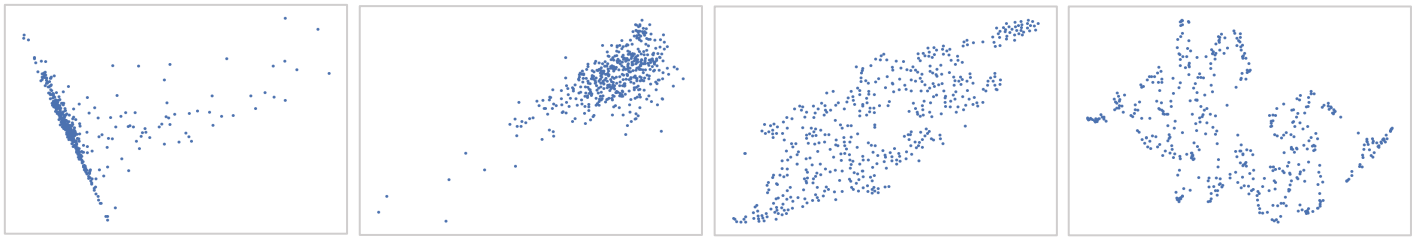

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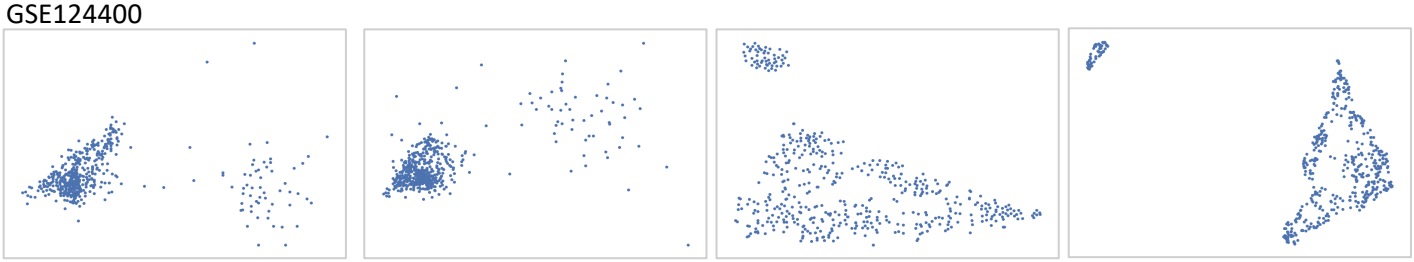

Figure S7: Gene set enrichment analysis between sG1 v.s. sG0 and sG2 v.s. sG0 with top 20 differentially regulated molecular pathways ranked by adjusted p-value.