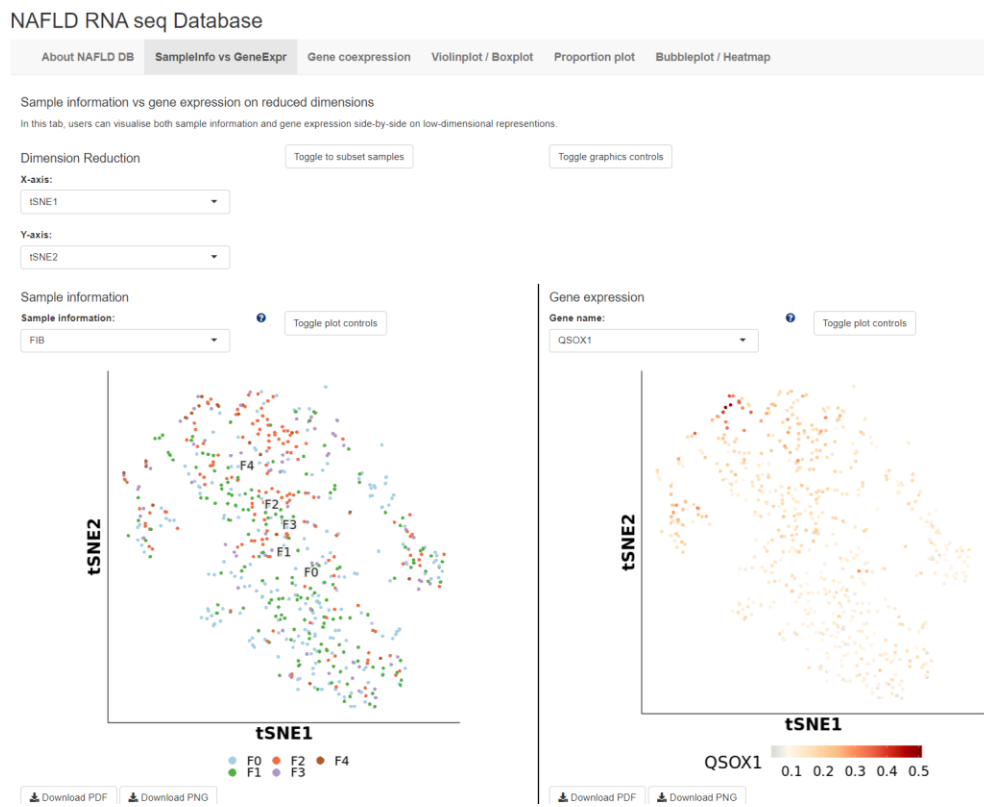


The database mainly contains five tabs (in grey panel) with interactive interface, with the opening page showing the first tab Sample Info vs GeneExpr (see below), plotting both cell information and gene expression side-by-side on reduced dimensions e.g. TSNE. Dimension reduction could be selected from PC, tSNE and UMAP by selecting from X-axis and Y-axis in “Dimension Reduction”. Samples color coding could be changed by selection of sample information.

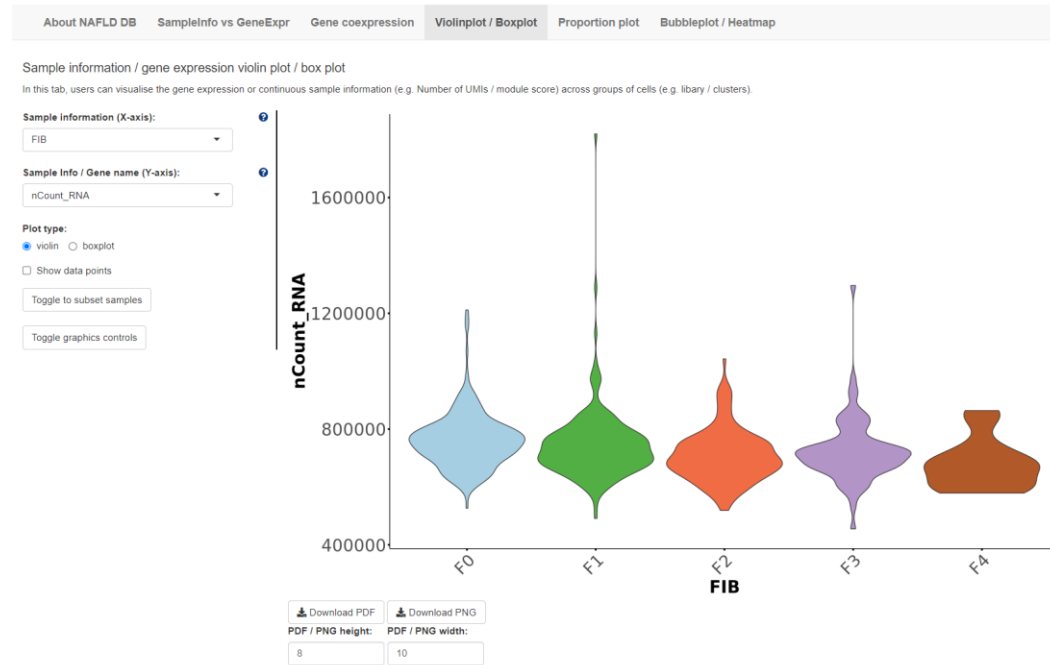
Samples could be subsetted with “Toggle to subset samples” bottom to select the groups of samples you would like to show. Plot could be adjusted with “Toggle plot control” bottom, including color, plot order etc. Point and font size could be changed with “Toggle graphic controls” bottom.

To select the gene of interest, simply type the first few letters in “Gene name” box and select from the list.



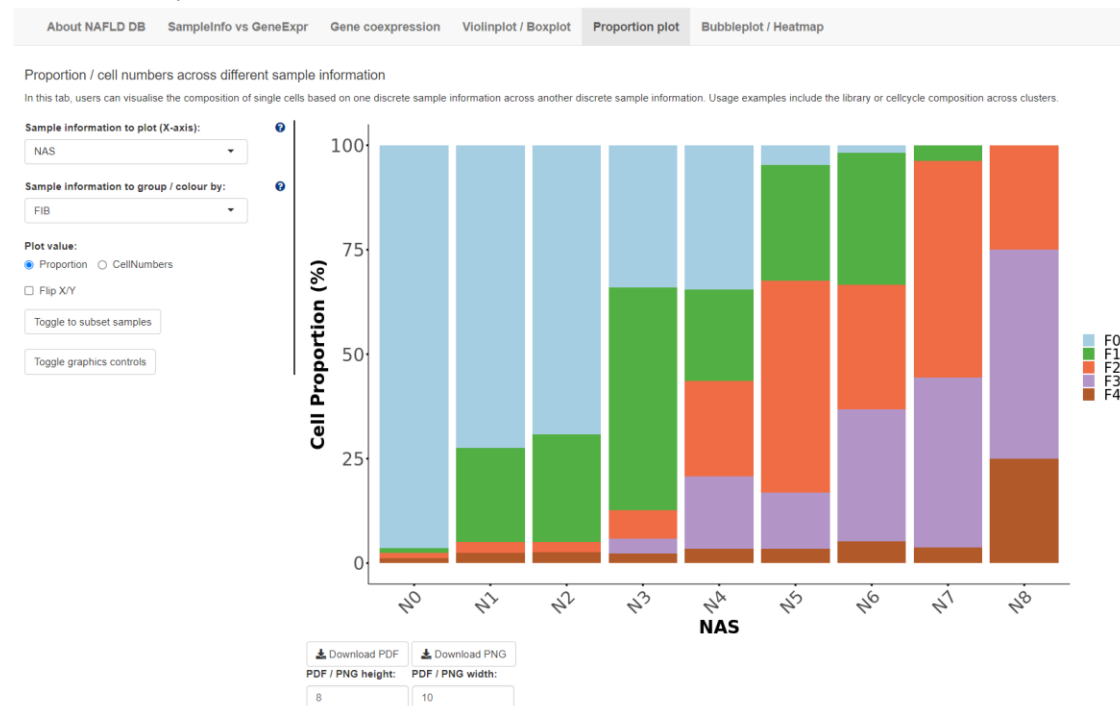
In Violinplot-Boxplot tab you could plots the distribution of continuous cell information e.g. nUMI or module scores or gene expression across each cluster / group using violin plots or box plots.

NAFLD RNA seq Database



In Proportion plot tab you could plots the composition of different clusters/groups of cells using proportion plots. Users can also plot the cell numbers instead of proportions.

NAFLD RNA seq Database



In Bubbleplot / Heatmap tab you could visualise the expression of multiple genes across each cluster / group using bubbleplots / heatmap. The genes (rows) and groups (columns) can be furthered clustered using hierarchical clustering.

NAFLD RNA seq Database

