

plot

plotQC

plotPCA - QC metrics

plotPCA - expression

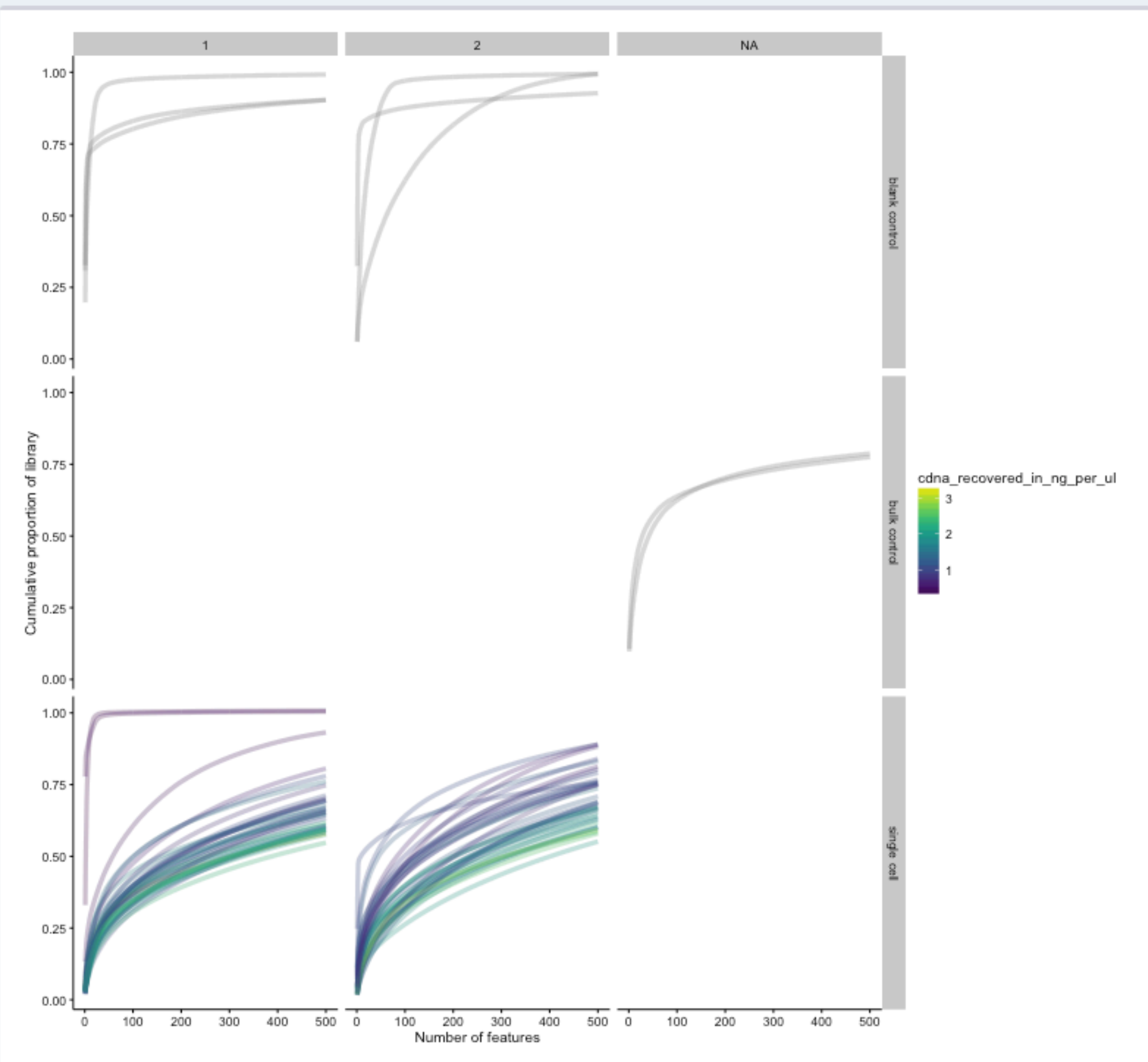
plotTSNE

plotDiffusionMap

plotExpression

## Overview of expression for each cell

Plots produced by this function are intended to provide an overview of large-scale differences between cells. For each cell, the features are ordered from most-expressed to least-expressed and the cumulative proportion of the total expression for the cell is computed across the top `nfeatures` features. These plots can flag cells with a very high proportion of the library coming from a small number of features; such cells are likely to be problematic for analyses. Using the colour and blocking arguments can flag overall differences in cells under different experimental conditions or affected by different batch and other variables.

**block1:**

c1\_machine ▼

**block2:**

well\_type ▼

**colour\_by:**

cdna\_recovered\_in\_ng\_per\_ul ▼

**exprs\_values:**

exprs ▼