

plot

plotQC

plotPCA - QC metrics

plotPCA - expression

plotTSNE

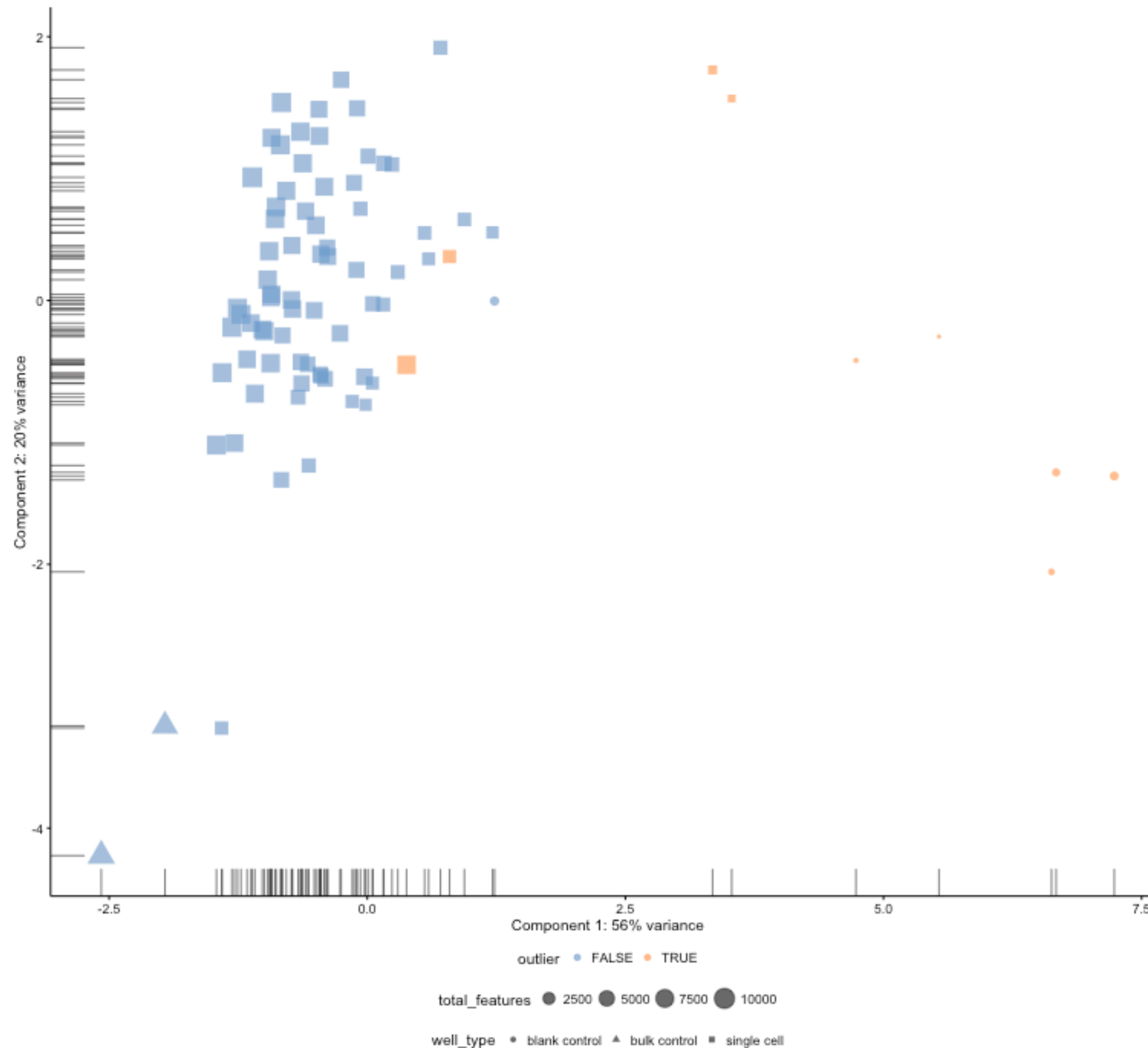
plotDiffusionMap

plotExpression

PCA using QC metrics and cell variables

Principal component analysis plots using QC metrics and cell metadata variables rather than expression levels. PCA on QC metrics can be used to identify potentially problematic cells, distinct from biological effects captured when using feature expression levels. See output in R session for names of detected outlier cells.

Points can be coloured either by cell metadata variables (see drop-down menus for shape_by and size_by for options) or feature expression levels, just enter a valid name into the text box below.

☒ detect outliers?

variables to use for PCA:

total_features pct_counts_feature_controls
pct_counts_top_100_features
n_detected_feature_controls
log10_counts_feature_controls
log10_counts_endogenous_features

colour_by (either cell metadata or feature expression):

c1_machine

shape_by:

well_type

size_by:

total_features

number of components:

2

☒ scale_features