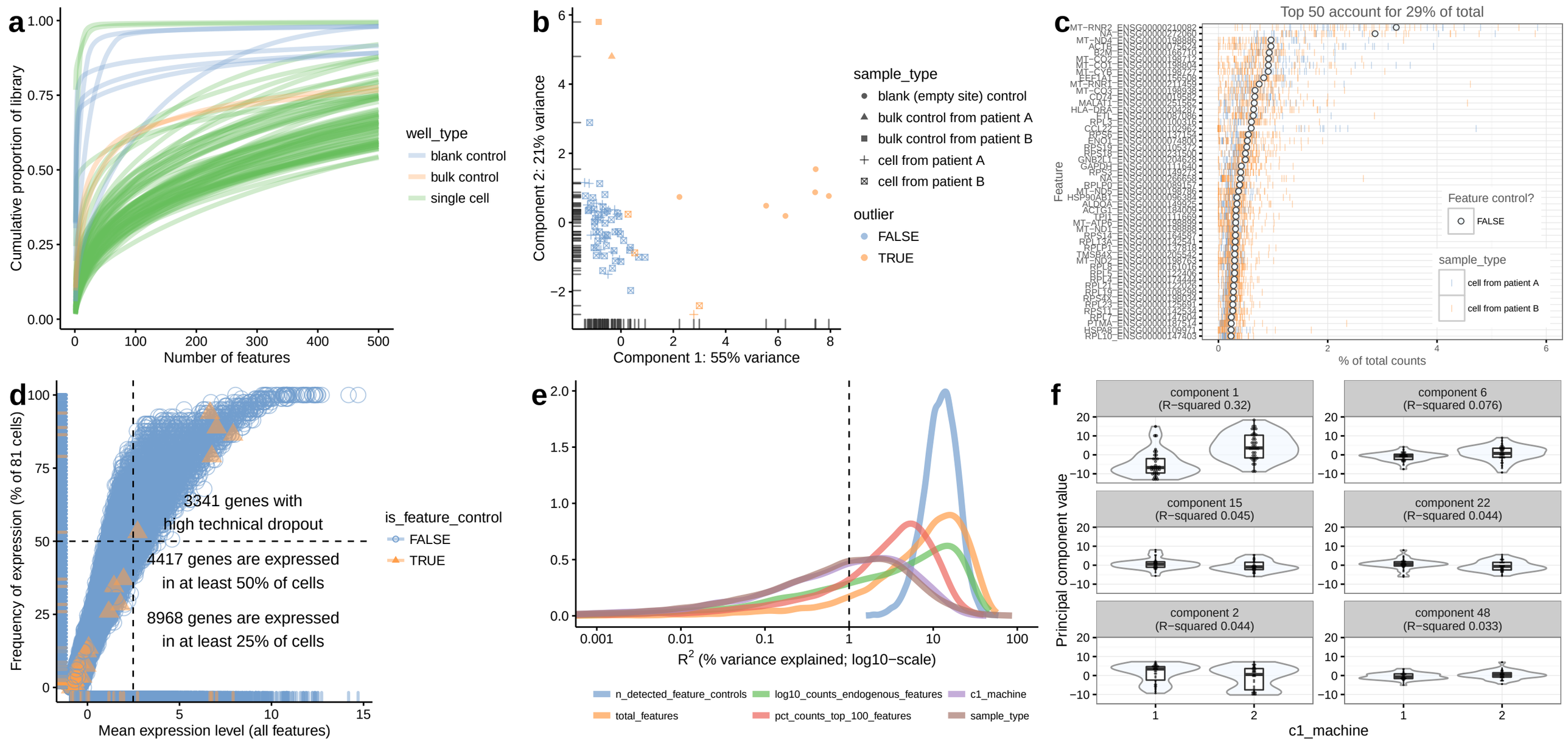
a
Cumulative proportion of library
Number of features
well_type
blank control
bulk control
single cell
b
Component 2: 21% variance
Component 1: 55% variance
sample_type
blank (empty site) control
bulk control from patient A
bulk control from patient B
cell from patient A
cell from patient B
outlier
FALSE
TRUE
c
Top 50 account for 29% of total
Feature
% of total counts
Feature control?
FALSE
sample_type
cell from patient A
cell from patient B
d
Frequency of expression (% of 81 cells)
Mean expression level (all features)
3341 genes with
high technical dropout
4417 genes are expressed
in at least 50% of cells
8968 genes are expressed
in at least 25% of cells
is_feature_control
FALSE
TRUE
e
R2 (% variance explained; log10−scale)
n_detected_feature_controls
log10_counts_endogenous_features
c1_machine
total_features
pct_counts_top_100_features
sample_type
f
Principal component value
component 1
(R−squared 0.32)
component 6
(R−squared 0.076)
component 15
(R−squared 0.045)
component 22
(R−squared 0.044)
component 2
(R−squared 0.044)
component 48
(R−squared 0.033)
c1_machine