<b>BATCH</b>	N_SAMPLES	N_CANCER	N_NORMAL
1	11	11	0
2	18	14	4
3	4	0	4
4	5	0	0
5	19	15	0

## **Key problems:**

## Imbalanced distribution:

Batches 1, 3, 5 are entirely composed of either cancer or normal samples -> It creates a strong association between batch and biological variables.

This can lead to confounding -> batch effects are misinterpreted as biological signals.

## Small sample sizes:

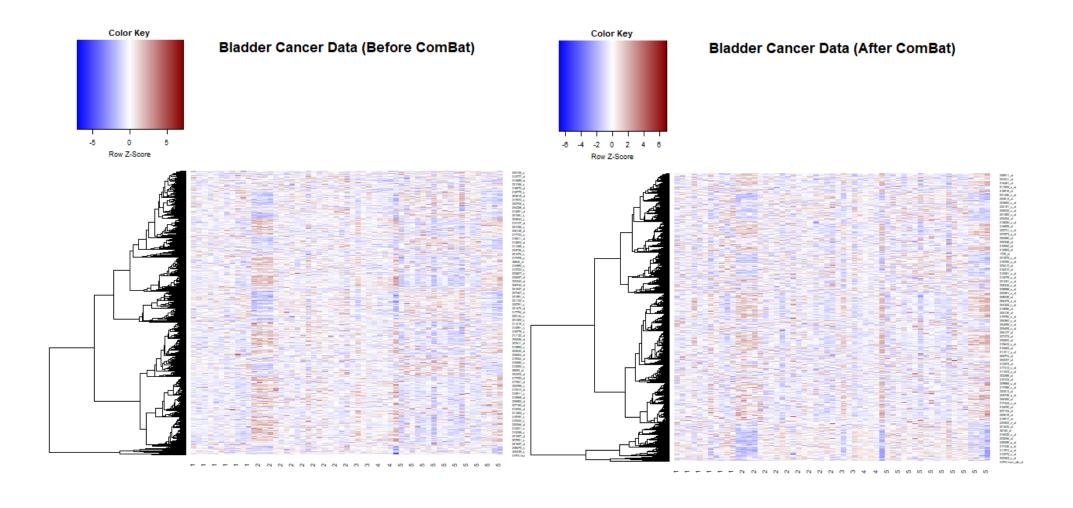
Batches 3, 4 have very few samples -> It reduce statistical power and increase the risk of overfitting.

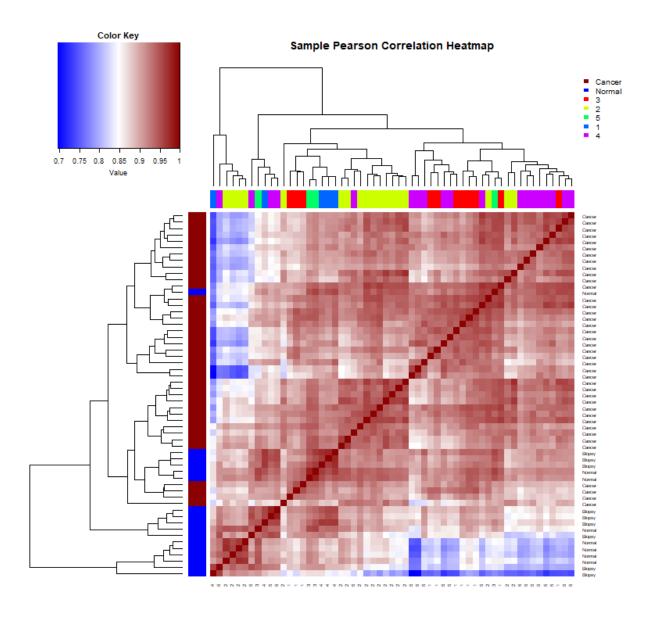
## Missing or mislabeled data:

Batch 4 contains no cancer or normal samples -> It suggests potential issues with data labeling or sample collection.

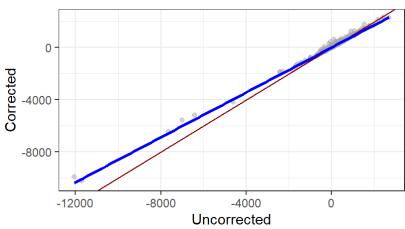
## Batch effects masking biological signals:

The strong association between batch and cancer status means that batch effects could mask true biological differences between cancer and normal samples.

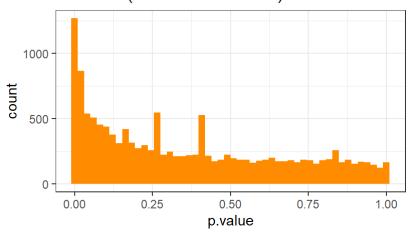








# P-values (Uncorrected Model)



# P-values (ComBat-Corrected Model)

