Identified proteins: \( n = 553 \)

Filter out: reverse proteins, usual contaminants and proteins only identified by site, \( n = 521 \)

Transform: \( \log_2(\text{LFQ}) \)

Filter valid hits and replace missing values:
- proteins identified with at least two values per group
- replace missing values from normal distribution
\( n = 329 \)

Multi-sample test

Two-samples tests:
- FDR = 0.05 and \( S_0 = 2 \)

Combination of all statistical tests: volcano plot
Proteins specific to RelAp43, \( n = 49 \)

Proteins specific to RelAp43, \( n = 49 \)

LFQ ratio Tha/CAT
- decreased by \( \text{M}_{\text{Tha}} (X < 0.5) \), \( n = 5 \)
- not affected by \( \text{M}_{\text{Tha}} \), \( n = 11 \)
- increased by \( \text{M}_{\text{Tha}} (X > 2) \), \( n = 33 \)