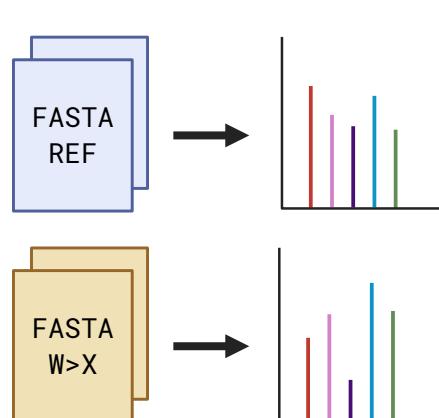
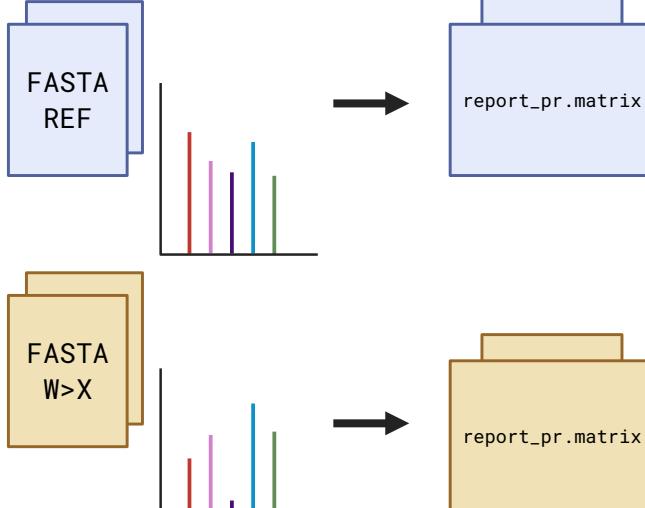


STEP 1

DIA-NN
Predicted spectral library generation

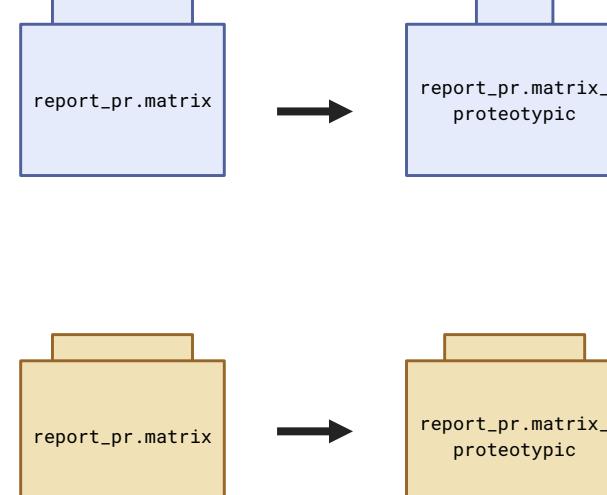


DIA-NN
Relative protein quantification



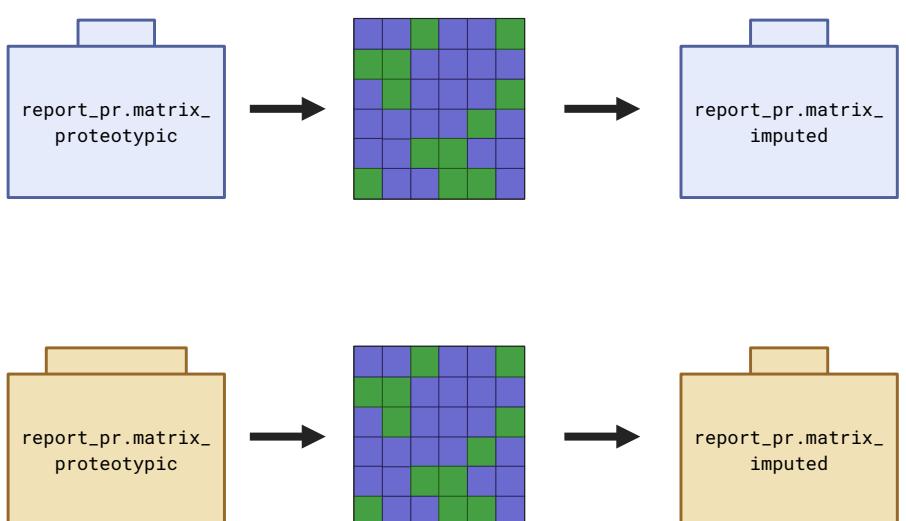
STEP 2

Perseus
Filter proteotypic values

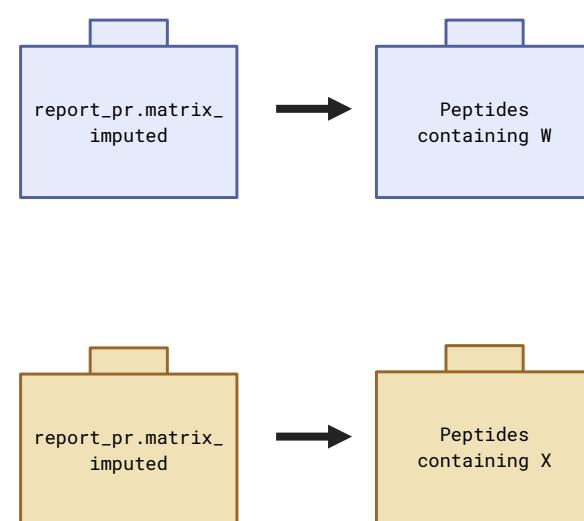


STEP 3

imputeLCMD - R
Impute missing values (impute.MinDet)



Perseus
Join datasets

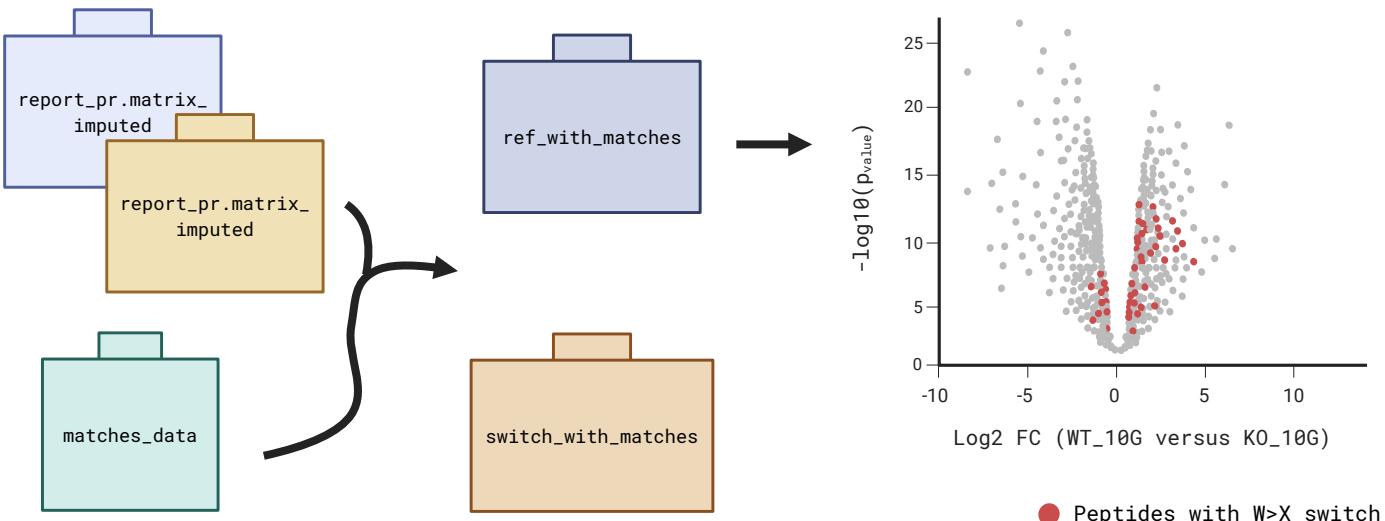


Excel
Search for presence of XXX(W/X)XXX peptides



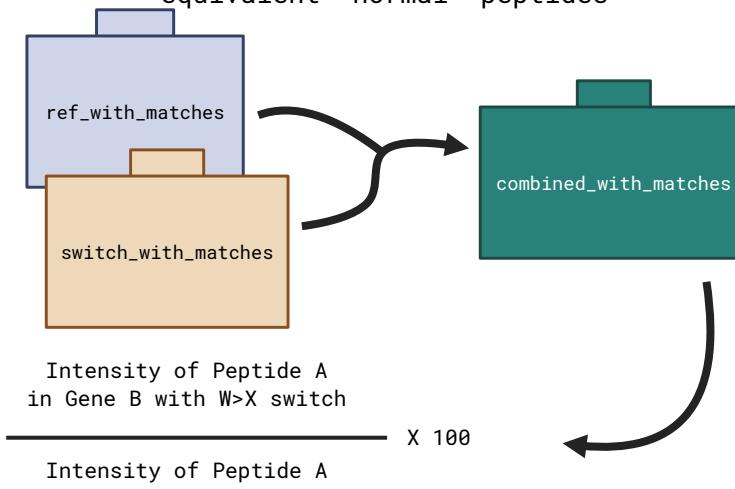
STEP 4

Perseus
Find (up/downregulated) proteins with a switched peptide



STEP 5

Perseus
Normalise abundance of switched peptides against equivalent "normal" peptides

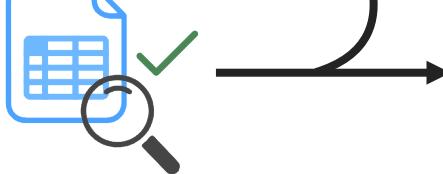


STEP 7

R
For each peptide, determine if there are significant differences in peptide abundance (as % of reference) between conditions of interest

ANOVA

ANOVA p >= 0.05



Tukey's HSD



Tukey's HSD p.adj >= 0.05

