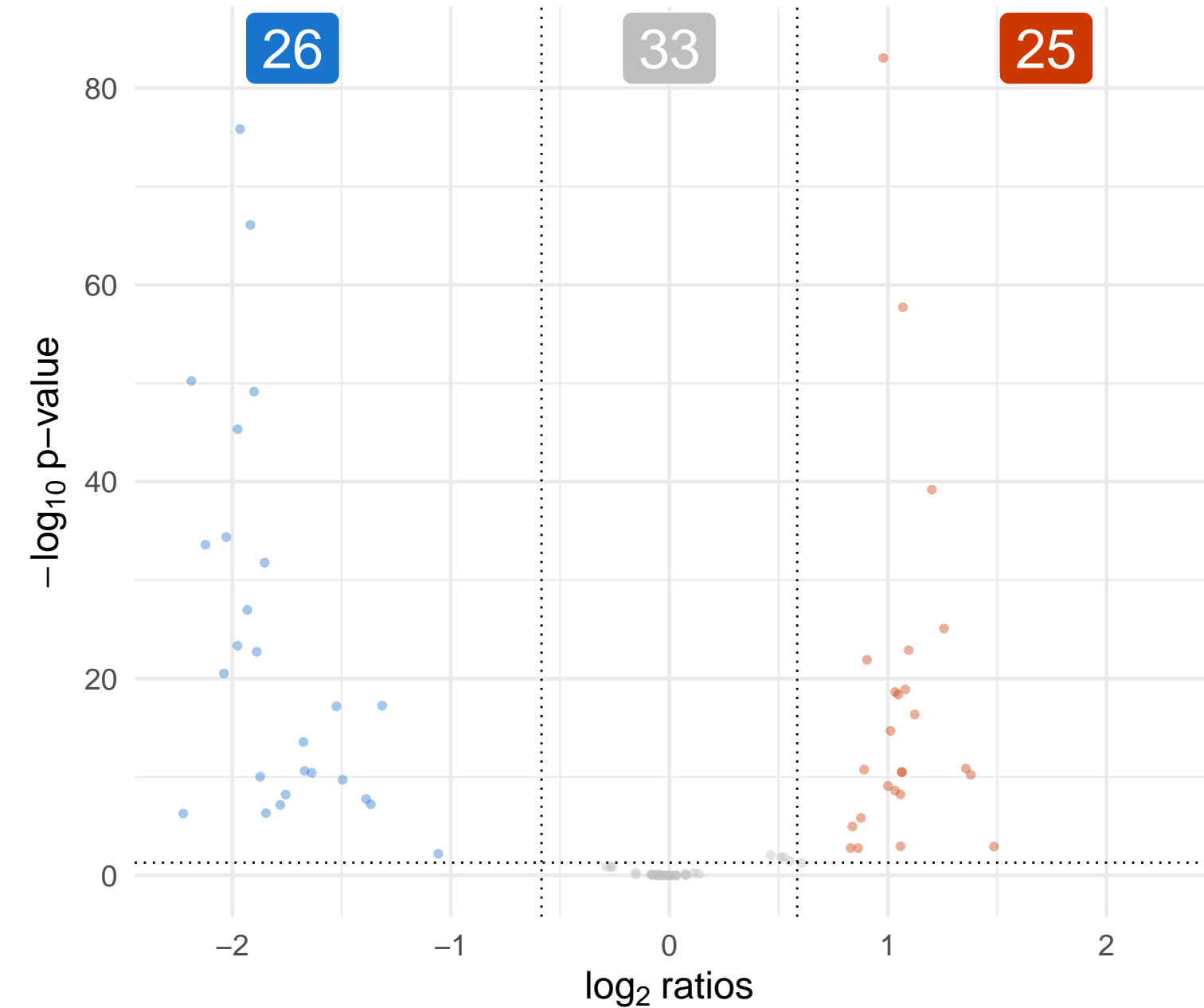


HYE mix A/
HYE mix B

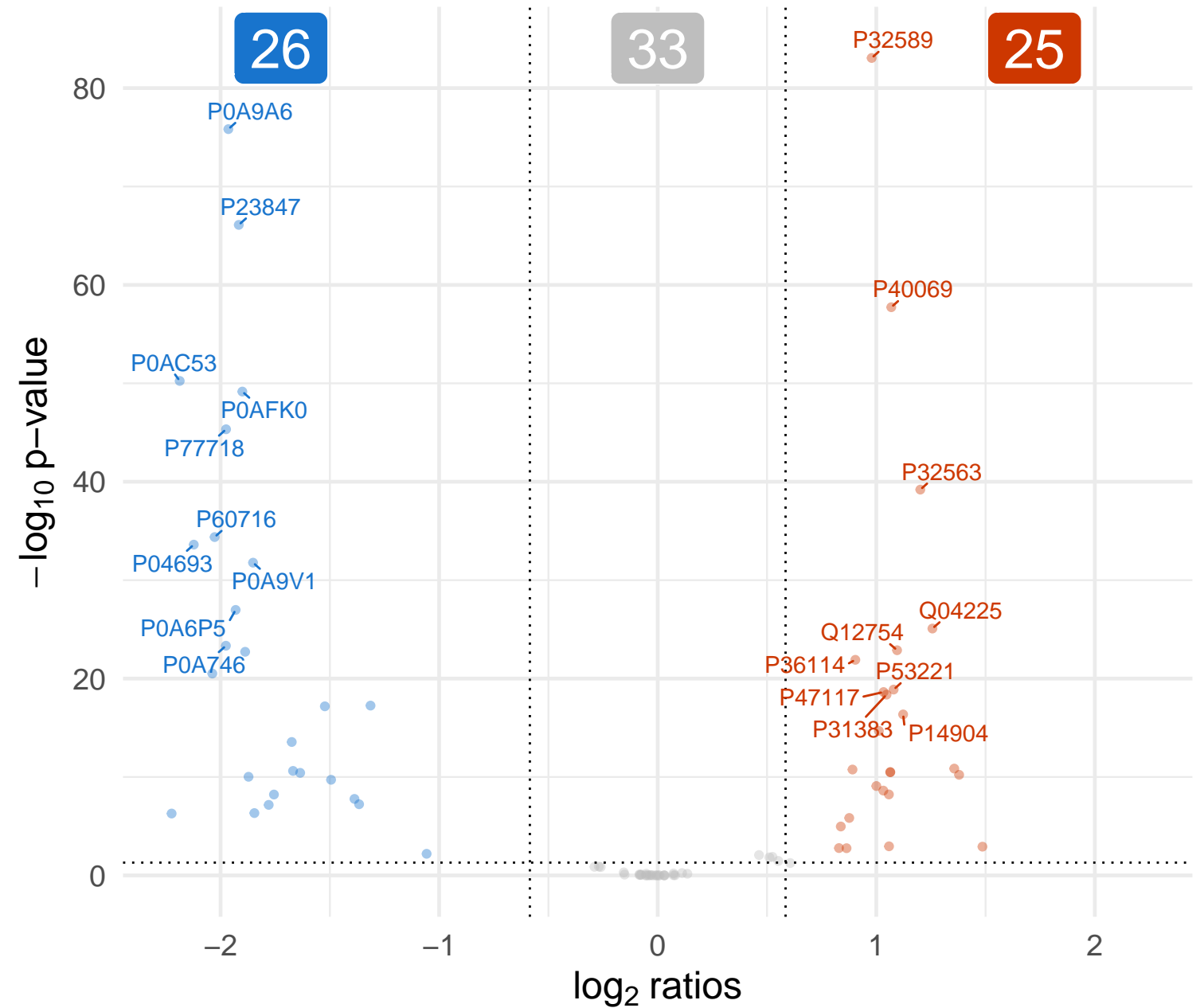
cutoffs: fold-change=1.5 / p-value=0.05



protein data filtered for equal or more 2 peptides

HYE mix A/
HYE mix B

cutoffs: fold-change=1.5 / p-value=0.05



protein data filtered for equal or more 2 peptides