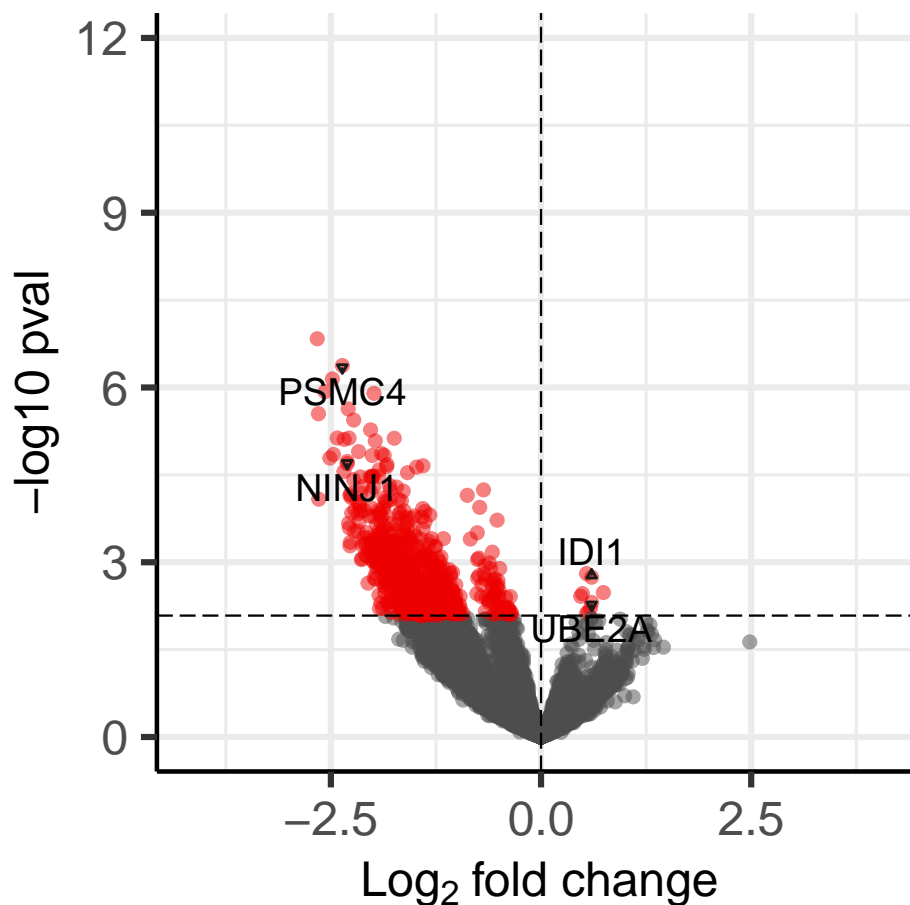


Ab > rest

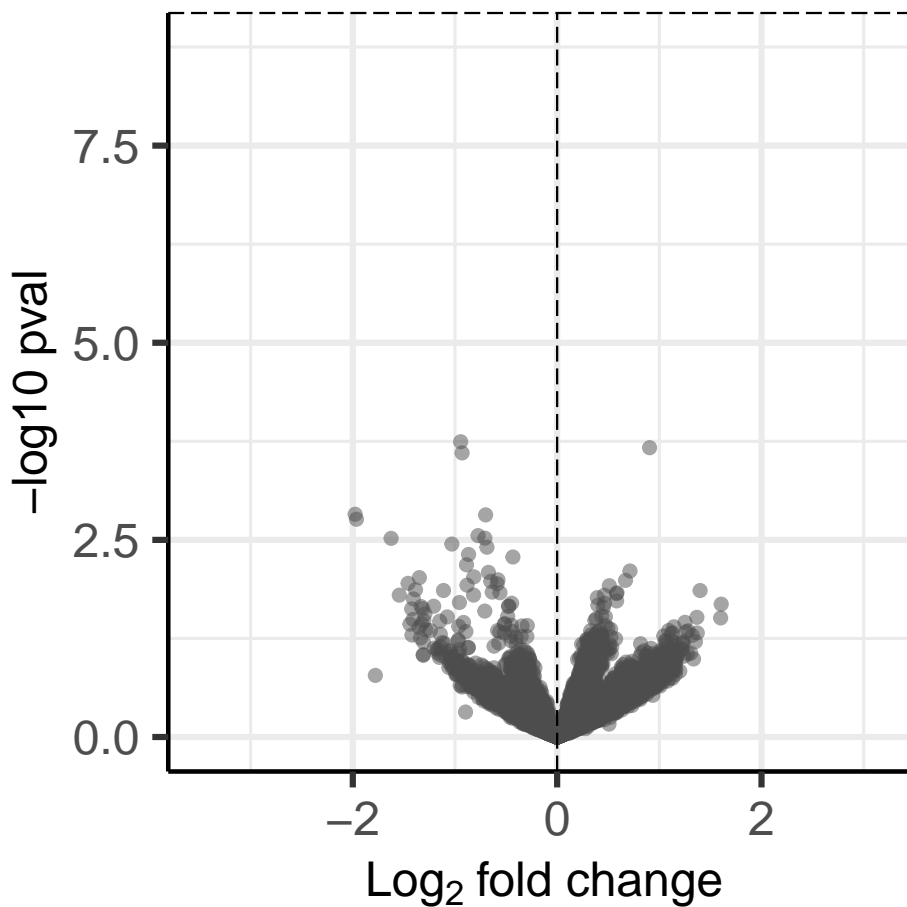
● Not sig. ● FDR < 0.1



total = 8443 genes

both > rest

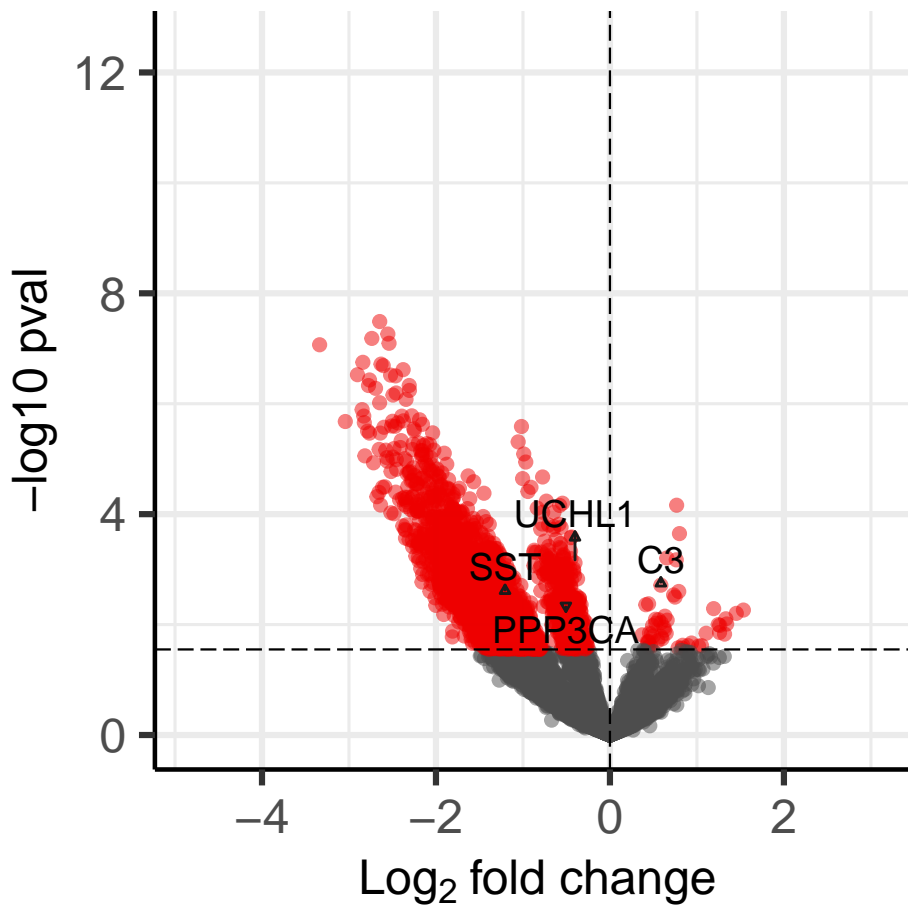
● Not sig.



total = 8443 genes

n_Ab > rest

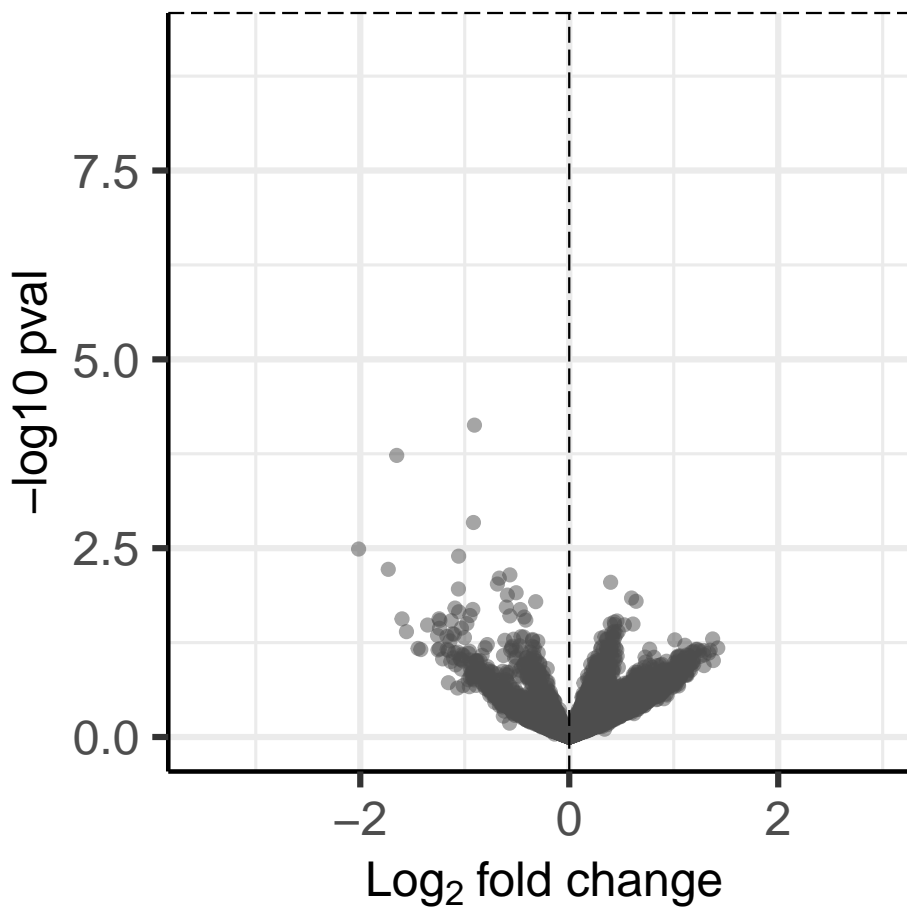
● Not sig. ● FDR < 0.1



total = 8443 genes

n_both > rest

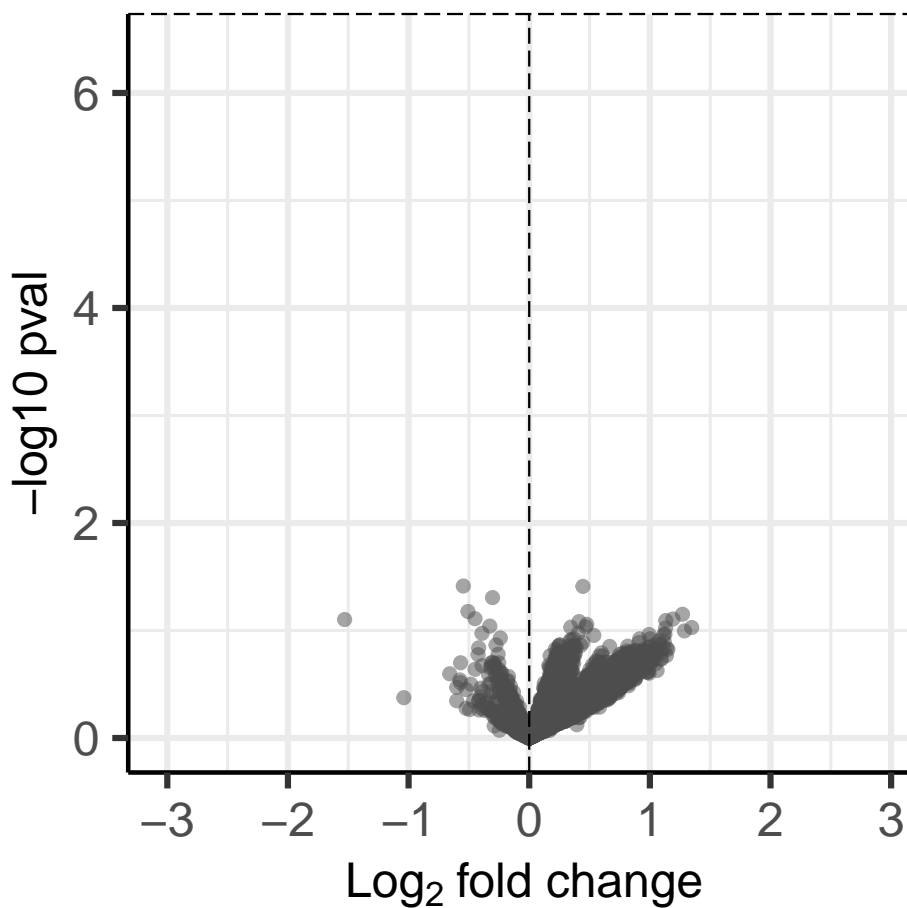
● Not sig.



total = 8443 genes

n_pTau > rest

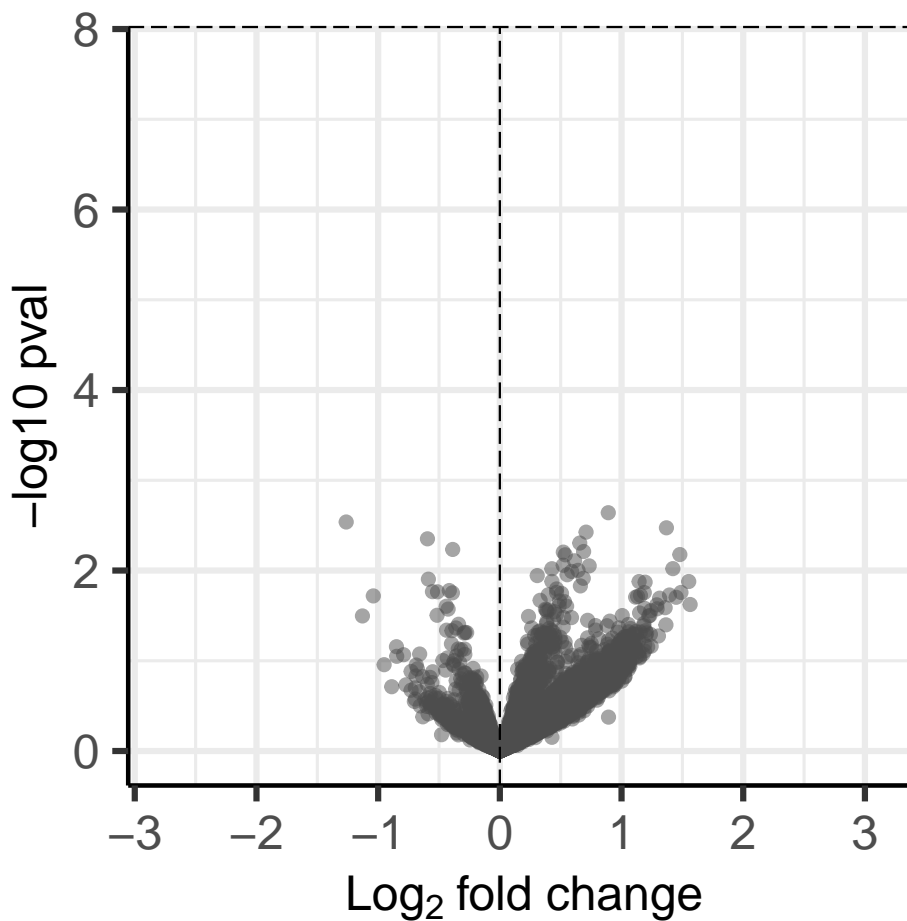
● Not sig.



total = 8443 genes

none > rest

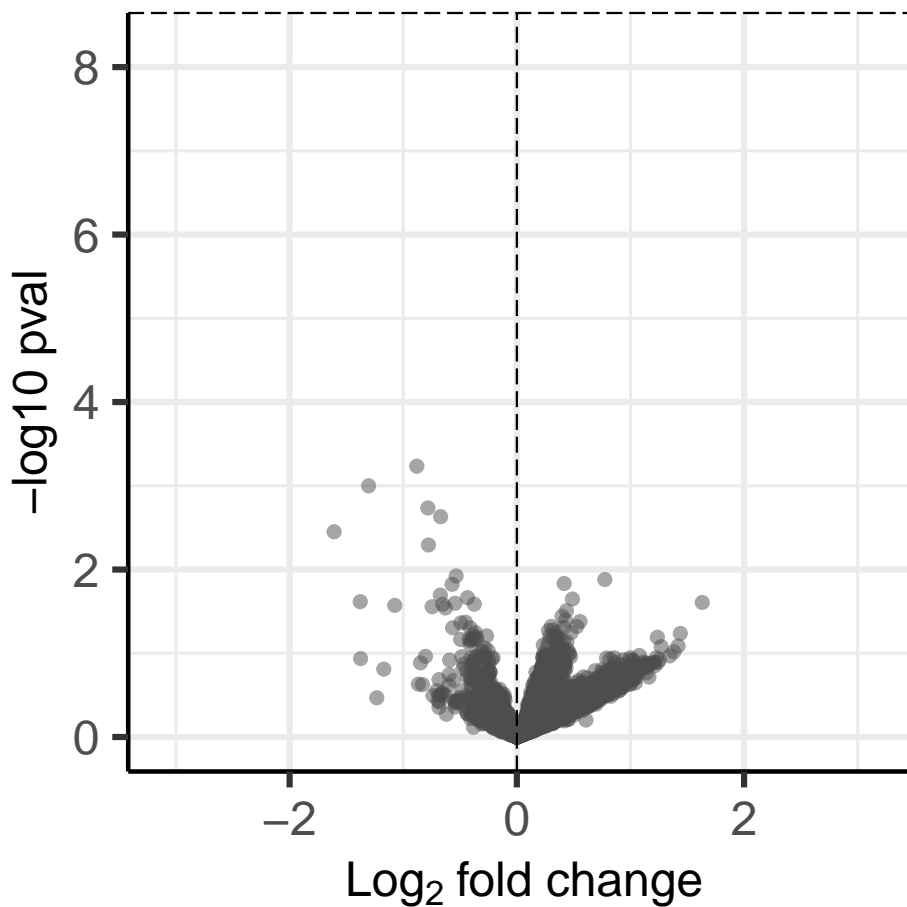
● Not sig.



total = 8443 genes

pTau > rest

● Not sig.



total = 8443 genes