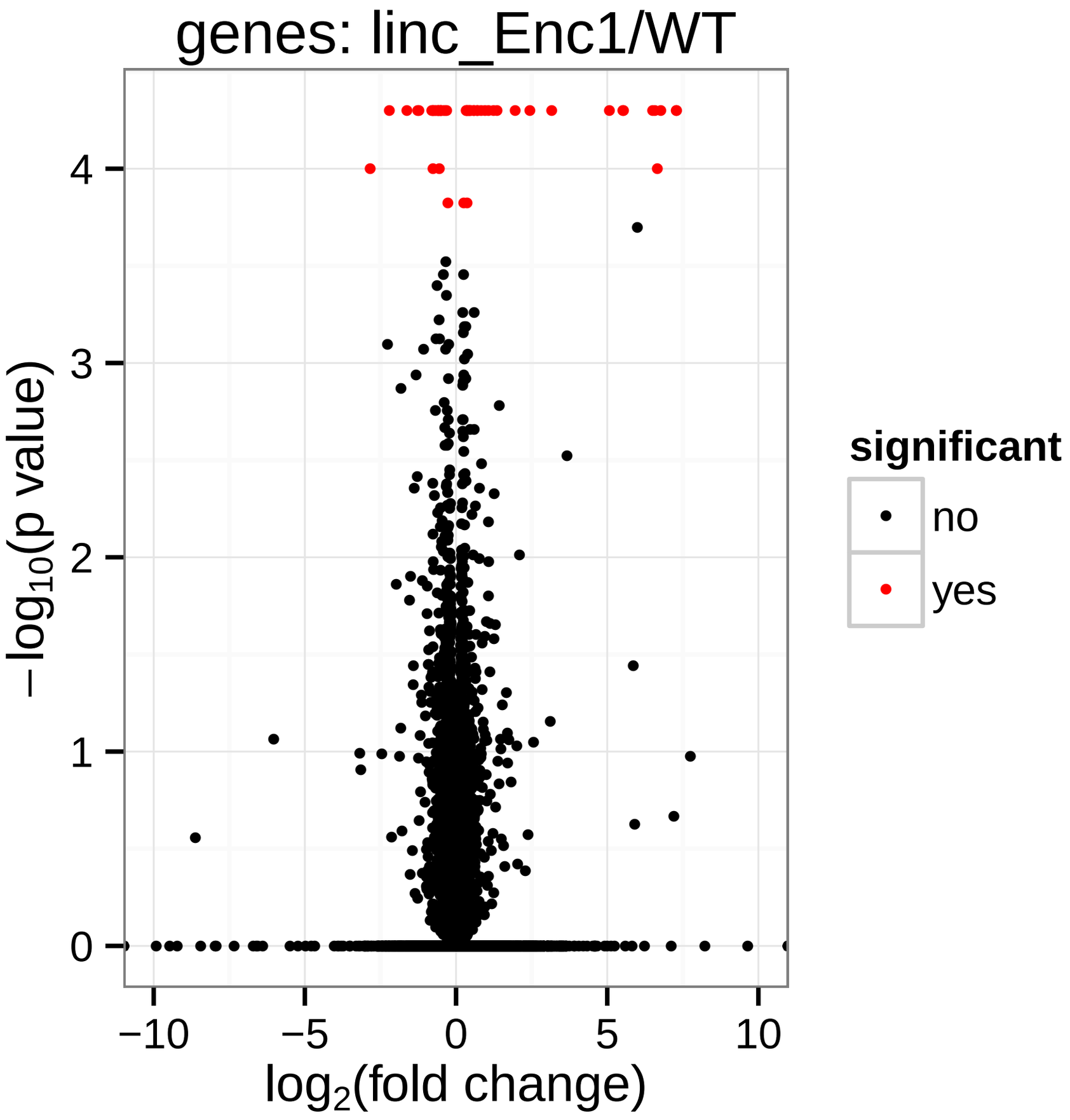
genes: linc_Enc1/WT
4
3
2
1
0
−log10(p value)
−10
−5
0
5
10
log2(fold change)
significant
no
yes